



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 143151**

**TO: Ruixiang Li**  
**Location: rem/4d75/4c70**  
**Art Unit: 1646**  
**Friday, February 11, 2005**

**Case Serial Number: 09/927267**

**From: Mary Jane Ruhl**  
**Location: Biotech-Chem Library**  
**Remsen 1-A-62**  
**Phone: 571-272-2524**

**maryjane.ruhl@uspto.gov**

### **Search Notes**

Examiner Li,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl  
Technical Information Specialist  
STIC  
Remsen 1-A-62  
Ext. 22524

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STIC-Biotech/ChemLib

143151

mg

From: Li, Ruixiang  
Sent: Tuesday, January 25, 2005 10:44 AM  
To: STIC-Biotech/ChemLib  
Subject: Sequence search of Application No.09/927,267

Please do a standard search on:

- (i). SEQ ID NOS: 1, 2, and 3 against interference nucleic acid databases;
- (ii). SEQ ID NO: 1 against interference amino acid databases.

Thank you very much!

Ruixiang Li  
GAU 1646  
REM 4D75  
Mail Box 4C70  
(571) 272-0875

RECEIVED  
JAN 25 2005  
STIC

\*\*\*\*\*

STAFF USE ONLY

Searcher: \_\_\_\_\_  
Searcher Phone: 2- \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search

NA Sequence: # \_\_\_\_\_  
AA Sequence: # \_\_\_\_\_  
Structure: # \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIS: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2005, 03:39:26 ; Search time 85 Seconds

(without alignments)  
2444.016 Million cell updates/sec

Title: US-09-927-267-1

Perfect score: 2989  
Sequence: 1 MSQDPRKVTSSPPAPSKA.....EGTSKDEGRASQEPPEPE 575

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database : Published Applications AA:\*

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2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
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19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*  
20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARYS

Result No.	Score	Query Match	Length	ID	Description
1	2989	100.0	575	9	US-09-735-932-2
2	2989	100.0	575	9	US-09-927-267-1
3	2989	100.0	575	14	US-10-207-951-2
4	2984	99.8	575	10	US-09-842-758-30
5	2984	99.8	575	15	US-10-174-333-30
6	2984	99.8	575	16	US-10-311-624-1
7	2957.5	98.9	578	10	US-09-842-758-28
8	2957.5	98.9	578	15	US-10-174-333-28
9	2811	94.0	575	9	US-09-735-932-4
10	2811	94.0	575	9	US-09-927-267-16
11	2811	94.0	575	9	US-09-842-758-74
12	2811	94.0	575	15	US-10-174-333-74
13	2394	80.1	1704	14	US-10-207-951-4

14	1568	52.5	663	14	US-10-029-677-16	Sequence 16, Appl
15	1565	52.4	664	14	US-10-295-573-5	Sequence 5, Appl
16	1562	52.3	664	9	US-09-735-927-4	Sequence 4, Appl
17	1562	52.3	732	10	US-09-842-758-73	Sequence 73, Appl
18	1562	52.3	732	10	US-10-029-677-15	Sequence 15, Appl
19	1562	52.3	732	15	US-10-174-333-73	Sequence 73, Appl
20	1558	52.1	664	14	US-10-029-677-18	Sequence 18, Appl
21	1558	52.1	664	14	US-10-087-217-2	Sequence 2, Appl
22	1558	52.1	664	14	US-10-295-573-8	Sequence 8, Appl
23	1554	52.0	664	14	US-10-295-573-7	Sequence 7, Appl
24	1554	52.0	664	14	US-10-087-217-6	Sequence 6, Appl
25	1554	52.0	664	14	US-10-295-573-6	Sequence 6, Appl
26	1549.5	51.8	694	10	US-09-842-758-75	Sequence 75, Appl
27	1549.5	51.8	694	11	US-09-855-828-14	Sequence 14, Appl
28	1549.5	51.8	694	14	US-10-345-680-26	Sequence 26, Appl
29	1549.5	51.8	694	15	US-10-174-333-75	Sequence 75, Appl
30	1549	51.8	664	14	US-10-087-217-4	Sequence 4, Appl
31	1547	51.8	664	14	US-10-029-677-17	Sequence 17, Appl
32	1545	51.7	664	14	US-10-087-217-8	Sequence 8, Appl
33	1538.5	51.5	690	11	US-09-855-828-15	Sequence 15, Appl
34	1535	51.4	664	9	US-09-735-927-2	Sequence 2, Appl
35	1535	51.4	664	13	US-10-034-843-2	Sequence 2, Appl
36	1535	51.4	664	14	US-10-168-651-7	Sequence 7, Appl
37	1535	51.4	664	14	US-10-114-153-18	Sequence 18, Appl
38	1532	51.3	664	14	US-10-029-677-24	Sequence 24, Appl
39	1529	51.2	664	14	US-10-029-677-2	Sequence 2, Appl
40	1208	40.4	239	14	US-10-189-507-10	Sequence 10, Appl
41	1196	40.0	239	14	US-10-189-507-6	Sequence 6, Appl
42	779	26.1	239	14	US-10-189-507-5	Sequence 5, Appl
43	773	25.9	239	14	US-10-189-507-9	Sequence 9, Appl
44	769	25.7	239	14	US-10-189-507-12	Sequence 12, Appl
45	655	21.9	809	11	US-09-855-828-1	Sequence 1, Appl

#### ALIGNMENTS

RESULT 1  
US-09-735-932-2  
Sequence 2, Application US/09735932  
Patent No. US20020037548A1  
GENERAL INFORMATION:  
APPLICANT: GUEGLER, Karl et al  
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUM AN TRANSPORTER PROTEINS,  
FILE REFERENCE: CL000663  
CURRENT APPLICATION NUMBER: US/09/735,932  
CURRENT FILING DATE: 2000-12-14  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 575  
TYPE: PRT  
ORGANISM: Human  
US-09-735-932-2

Query Match 100.0%, Score 2989, DB 9, Length 575;  
Best Local Similarity 100.0%, Pred. No. 1.7e-253;  
Matches 575; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MSQDPRKVTSSPPAPSKAR	KL	PVLPDSGGYYWMLNTW	F	PVWYNLI	IVCRACFPD	60
DB	1	MSQDPRKVTSSPPAPSKAR	KL	LVDPDSGYIYWMNTW	F	PVWYNLI	IVCRACFPD	60
QY	61	LOHGYLVAMLVLDYTS	LDL	YVVRPHGTGLEGGI	LV	VDKGRIS	SRVRTWSEFLDIA	120
DB	61	LOHGYLVAMLVLDYTS	LDL	YVVRPHGTGLEGGI	LV	VDKGRIS	SRVRTWSEFLDIA	120
QY	121	SIMPTDVVYVRLGPH	PTLR	LRFLRPA	RF	FAFRTERT	RYAFA	180
DB	121	SIMPTDVVYVRLGPH	PTLR	LRFLRPA	RF	FAFRTERT	RYAFA	180
QY	121	SIMPTDVVYVRLGPH	PTLR	LRFLRPA	RF	FAFRTERT	RYAFA	180
DB	121	SIMPTDVVYVRLGPH	PTLR	LRFLRPA	RF	FAFRTERT	RYAFA	180

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Db 181 HNSCLYFALSRYLGFGRDAWVYPPAOPGFERLRQYLYSEFYSTLLITTVGDTPEPPAR 240
QY 241 EEEYLFMWGDFLLAVWGFAITMGSSSVIYNNMTADAAFPYDHALYKCYMKLOHVNRKLE 300
Db 241 EEEYLFMWGDFLLAVWGFAITMGSSSVIYNNMTADAAFPYDHALYKCYMKLOHVNRKLE 300
QY 301 RRVIDMYOHLQINKKMTNEVALIQLHLPRLRAEVAVSHLSTLSRVQIFONCEASLLEEL 360
Db 301 RRVIDMYOHLQINKKMTNEVALIQLHLPRLRAEVAVSHLSTLSRVQIFONCEASLLEEL 360
QY 361 VLKLOPQYTSPEGYVCRKDGIGQEMYIIREGQLAVVADGITOYAVLAGLYFGEISITIN 420
Db 361 VLKLOPQYTSPEGYVCRKDGIGQEMYIIREGQLAVVADGITOYAVLAGLYFGEISITIN 420
QY 421 IKGNMGNRRNTANIKSLGYSDLPCLSKEDLREVLSEYPOAQTIMEKREILLKNNKLDV 480
Db 421 IKGNMGNRRNTANIKSLGYSDLPCLSKEDLREVLSEYPOAQTIMEKREILLKNNKLDV 480
QY 481 NAEAEIALQEAATESRLRGDQDLDTQTKFARLLAELESSALKIAYRIERLEMOTREMP 540
Db 481 NAEAEIALQEAATESRLRGDQDLDTQTKFARLLAELESSALKIAYRIERLEMOTREMP 540
QY 541 MPEDLAADDEGPEBEGTSKDEBGRASQEGPPGPE 575
Db 541 MPEDLAADDEGPEBEGTSKDEBGRASQEGPPGPE 575
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RESULT 2  
US-09-927-267-1

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/ Sequence 1, Application US/09977267
/ Publication No. US20020182691A1
/ GENERAL INFORMATION:
/ APPLICANT: Crech, Christopher D.
/ APPLICANT: Jegla, Timothy J.
/ APPLICANT: ICAGEN, Inc.
/ TITLE OF INVENTION: CNG2B. A No. US20020182691A1 Human Cyclic Nucleotide-Gated Ion
/ TITLE OF INVENTION: Channel
/ FILE REFERENCE: 018512-006510US
/ CURRENT APPLICATION NUMBER: US/09/927,267
/ CURRENT FILING DATE: 2001-08-10
/ PRIOR APPLICATION NUMBER: US 60/226,253
/ PRIOR FILING DATE: 2000-08-17
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 1
/ LENGTH: 575
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: cyclic nucleotide-gated cation channel 2B (CNG2B)
US-09-927-267-1
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Query Match 100.0%; Score 2989; DB 9; Length 575;  
Best Local Similarity 100.0%; Pred. No. 1.7e-253;

Matches 575; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MSODTKVKTTESSPPAPSKARKLLPVLDPSGDYIYMWLNTMVPVYNNLIILVCRACFPD 60
QY 61 LOHGIVLAVMLVLDYSDLLYLDMVVRPHFTGFLGQGLIVVDKRRISRYRTWSFFLDLA 120
Db 61 LOHGIVLAVMLVLDYSDLLYLDMVVRPHFTGFLGQGLIVVDKRRISRYRTWSFFLDLA 120
QY 121 SLMPDVVVYRLGPHPTLRINRFLAPRLFEAFDRTEFTRTAYNAPRIAKMLYIFVVI 180
Db 121 SLMPDVVVYRLGPHPTLRINRFLAPRLFEAFDRTEFTRTAYNAPRIAKMLYIFVVI 180
QY 181 HNSCLYFALSRYLGFGRDAWVYPPAOPGFERLRQYLYSEFYSTLLITTVGDTPEPPAR 240
Db 181 HNSCLYFALSRYLGFGRDAWVYPPAOPGFERLRQYLYSEFYSTLLITTVGDTPEPPAR 240
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Db 241 EEEYLFMWGDFLLAVWGFAITMGSSSVIYNNMTADAAFPYDHALYKCYMKLOHVNRKLE 300
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Db 241 EEEYLFMWGDFLLAVWGFAITMGSSSVIYNNMTADAAFPYDHALYKCYMKLOHVNRKLE 300
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Db 301 RRVIDMYOHLQINKKMTNEVALIQLHLPRLRAEVAVSHLSTLSRVQIFONCEASLLEEL 360
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Db 361 VLKLOPQYTSPEGYVCRKDGIGQEMYIIREGQLAVVADGITOYAVLAGLYFGEISITIN 420
QY 421 IKGNMGNRRNTANIKSLGYSDLPCLSKEDLREVLSEYPOAQTIMEKREILLKNNKLDV 480
Db 421 IKGNMGNRRNTANIKSLGYSDLPCLSKEDLREVLSEYPOAQTIMEKREILLKNNKLDV 480
QY 481 NAEAEIALQEAATESRLRGDQDLDTQTKFARLLAELESSALKIAYRIERLEMOTREMP 540
Db 481 NAEAEIALQEAATESRLRGDQDLDTQTKFARLLAELESSALKIAYRIERLEMOTREMP 540
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Db 541 MPEDLAADDEGPEBEGTSKDEBGRASQEGPPGPE 575
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RESULT 3  
US-10-207-951-2

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/ Sequence 2, Application US/10207951
/ Publication No. US20030013156A1
/ GENERAL INFORMATION:
/ APPLICANT: Karl GUEGLER et al.
/ TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
/ TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS
/ TITLE OF INVENTION: AND USUS THEREOF
/ FILE REFERENCE: CL000663CON
/ CURRENT APPLICATION NUMBER: US/10/207,951
/ CURRENT FILING DATE: 2002-07-31
/ PRIOR APPLICATION NUMBER: 09/735,932
/ PRIOR FILING DATE: 2000-12-14
/ PRIOR APPLICATION NUMBER: 60/211,223
/ PRIOR FILING DATE: 2000-06-13
/ NUMBER OF SEQ ID NOS: 25
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2
/ LENGTH: 575
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-207-951-2
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Query Match 100.0%; Score 2989; DB 14; Length 575;  
Best Local Similarity 100.0%; Pred. No. 1.7e-253;

Matches 575; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 LOHGIVLAVMLVLDYSDLLYLDMVVRPHFTGFLGQGLIVVDKRRISRYRTWSFFLDLA 120
QY 121 SLMPDVVVYRLGPHPTLRINRFLAPRLFEAFDRTEFTRTAYNAPRIAKMLYIFVVI 180
Db 121 SLMPDVVVYRLGPHPTLRINRFLAPRLFEAFDRTEFTRTAYNAPRIAKMLYIFVVI 180
QY 181 HNSCLYFALSRYLGFGRDAWVYPPAOPGFERLRQYLYSEFYSTLLITTVGDTPEPPAR 240
Db 181 HNSCLYFALSRYLGFGRDAWVYPPAOPGFERLRQYLYSEFYSTLLITTVGDTPEPPAR 240
QY 241 EEEYLFMWGDFLLAVWGFAITMGSSSVIYNNMTADAAFPYDHALYKCYMKLOHVNRKLE 300
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DB 301 REVIMWYOHLOINKMTNEVALLOHLPERLRAEVAVSHLSTLSRVQIFONCEASLLEEL 360  
QY 361 VKLQPOPTYSPEYVCRKGDIGQEWYIIREGOLAVVADGITOYAVLAGLYFGEISIIIN 420  
DB 361 VKLQPOPTYSPEYVCRKGDIGQEWYIIREGOLAVVADGITOYAVLAGLYFGEISIIIN 420  
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DB 421 IKGNNSGNRRNTANIKSLGSDLFCLSKEDLREVLSEYPOAQITMEKREIILKNKLDV 480  
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DB 481 NAEAEIALQEAATESRLRGDLODDLOTKFARLLAELESSALKIAYRIERLEWOTREMP 540  
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DB 541 MPEDLAADDEGEPEEGTSKDEEGRASOGPPGPE 575

## RESULT 4

US-09-842-758-30  
Sequence 30, Application US/09842758  
Publication No. US20030083244A1  
GENERAL INFORMATION:  
APPLICANT: Vernet, Corine A. M.  
APPLICANT: Fernandes, Elma R.  
APPLICANT: Gerlach, Valerie  
APPLICANT: Shinkens, Richard A.  
APPLICANT: Malynkar, Uriel M.  
APPLICANT: Boldog, Ferenc L.  
APPLICANT: Zehnusen, Bryan D.  
APPLICANT: Spytek, Kimberly A.  
APPLICANT: Majumder, Kumud  
APPLICANT: Tchernev, Velizar T.  
APPLICANT: Padigaru, Muralidhara  
APPLICANT: Patturajan, Meera  
APPLICANT: Burgess, Catherine E.  
APPLICANT: Gangoli, Bsha A.  
APPLICANT: Smithson, Glenda  
APPLICANT: Raetelli, Luca  
APPLICANT: MacDougall, John R.  
APPLICANT: Taupier, Raymond J.  
APPLICANT: Groese, William M.  
APPLICANT: Edward, Szekeres S.  
APPLICANT: Alsbrook II, John P.  
TITLE OF INVENTION: No. US20030083244A1e1 Proteins and Nucleic Acids Encoding Same  
FILE REFERENCE: 15966-783  
CURRENT APPLICATION NUMBER: US/09/842,758  
CURRENT FILING DATE: 2001-04-25  
PRIOR APPLICATION NUMBER: 60/200,158  
PRIOR FILING DATE: 2000-04-26  
PRIOR APPLICATION NUMBER: 60/200,613  
PRIOR FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: 60/200,780  
PRIOR FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: 60/201,006  
PRIOR FILING DATE: 2000-05-01  
PRIOR APPLICATION NUMBER: 60/201,007  
PRIOR FILING DATE: 2000-05-01  
PRIOR APPLICATION NUMBER: 60/201,236  
PRIOR FILING DATE: 2000-05-01  
PRIOR APPLICATION NUMBER: 60/201,238  
PRIOR FILING DATE: 2000-05-01  
PRIOR APPLICATION NUMBER: 60/201,186  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 60/201,474  
PRIOR FILING DATE: 2000-05-03  
PRIOR APPLICATION NUMBER: 60/201,508  
PRIOR FILING DATE: 2000-05-03  
PRIOR APPLICATION NUMBER: 60/220,591

PRIOR FILING DATE: 2000-07-25  
PRIOR APPLICATION NUMBER: 60/232,678  
PRIOR FILING DATE: 2000-09-15  
PRIOR APPLICATION NUMBER: 60/263,217  
PRIOR FILING DATE: 2001-01-22  
PRIOR APPLICATION NUMBER: 60/265,160  
PRIOR FILING DATE: 2001-01-30  
NUMBER OF SEQ ID NOS: 113  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO: 30  
LENGTH: 575  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-842-758-30

Query Match 99.8%; Score 2984; DB 10; Length 575;  
Best Local Similarity 99.8%; Pred. No. 4,8e-253; Indels 0; Gaps 0;  
Matches 574; Conservative 0; Mismatches 1;

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DB 1 MSQDTKVTTESSPPAPSKARKLPLVDPSSGDYYWMIINTWVFPVMNLIILVCRACFPD 60  
QY 61 LQHGVLVAMLVLDYTSLLYLLDMVVRPHGTFLEQGIIVDKRISRRVRTWSPFLDLA 120  
DB 61 LQHGVLVAMLVLDYTSLLYLLDMVVRPHGTFLEQGIIVDKRISRRVRTWSPFLDLA 120  
QY 121 SLMPDVTYVYVRLGPTPLRLNRFARPLPEAPRTETRTAYPAFPAKMLYIPVYI 180  
DB 121 SLMPDVTYVYVRLGPTPLRLNRFARPLPEAPRTETRTAYPAFPAKMLYIPVYI 180  
QY 181 HNSCLYFALSRYLGFGRDAMWYPPDAPGFERLRQYLYSFYSTLLITTVGDTPPPAR 240  
DB 181 HNSCLYFALSRYLGFGRDAMWYPPDAPGFERLRQYLYSFYSTLLITTVGDTPPPAR 240  
QY 241 EEEYLFMYGDFLLAVMGFATTMGSSSVIYNNMTADAAFPYDHALVKKYMKLOHYNRKLE 300  
DB 241 EEEYLFMYGDFLLAVMGFATTMGSSSVIYNNMTADAAFPYDHALVKKYMKLOHYNRKLE 300  
QY 301 RRVIMWYOHLOINKMTNEVALLOHLPERLRAEVAVSHLSTLSRVQIFONCEASLLEEL 360  
DB 301 RRVIMWYOHLOINKMTNEVALLOHLPERLRAEVAVSHLSTLSRVQIFONCEASLLEEL 360  
QY 361 VKLQPOPTYSPEYVCRKGDIGQEWYIIREGOLAVVADGITOYAVLAGLYFGEISIIIN 420  
DB 361 VKLQPOPTYSPEYVCRKGDIGQEWYIIREGOLAVVADGITOYAVLAGLYFGEISIIIN 420  
QY 421 IKGNNSGNRRNTANIKSLGSDLFCLSKEDLREVLSEYPOAQITMEKREIILKNKLDV 480  
DB 421 IKGNNSGNRRNTANIKSLGSDLFCLSKEDLREVLSEYPOAQITMEKREIILKNKLDV 480  
QY 481 NAEAEIALQEAATESRLRGDLODDLOTKFARLLAELESSALKIAYRIERLEWOTREMP 540  
DB 481 NAEAEIALQEAATESRLRGDLODDLOTKFARLLAELESSALKIAYRIERLEWOTREMP 540  
QY 541 MPEDLAADDEGEPEEGTSKDEEGRASOGPPGPE 575  
DB 541 MPEDLAADDEGEPEEGTSKDEEGRASOGPPGPE 575

## RESULT 5

US-10-174-333-30  
Sequence 30, Application US/10174333  
Publication No. US20040029220A1  
GENERAL INFORMATION:  
APPLICANT: Vernet, Corine A. M.  
APPLICANT: Fernandes, Elma R.  
APPLICANT: Gerlach, Valerie  
APPLICANT: Malynkar, Uriel M.  
APPLICANT: Boldog, Ferenc L.  
APPLICANT: Zehnusen, Bryan D.  
APPLICANT: Spytek, Kimberly A.  
APPLICANT: Majumder, Kumud

```

; APPLICANT: Tchernov, Velizar T.
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Paturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Gangoli, Raha A.
; APPLICANT: Smithson, Glenda
; APPLICANT: Rastelli, Luca
; APPLICANT: MacDougall, John R.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Grose, William M.
; APPLICANT: Szekeres, Edward S.
; APPLICANT: Alsobrook, John P.
; APPLICANT: Anderson, David M.
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Li, Li
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-783 CIP1
; CURRENT APPLICATION NUMBER: US/10/174,333
; PRIOR FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 60/193,664
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 60/194,614
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 60/195,063
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,066
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,067
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,068
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,069
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,070
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,510
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/219,855
; PRIOR FILING DATE: 2000-07-21
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: Cytosql version 0.1
; SEQ ID NO 30
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-174-333-30
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Query Match          99.8%; Score 2984; DB 15; Length 575;
Best Local Similarity 99.8%; Pred. No. 4.8e-253;
Matches 574; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSODTKVKTSSPPAPSKARKLLPVLDPSGDYVYMWLNTMVPVWYNIILVCRACFPD 60
DB 1 MSODTKVKTSSPPAPSKARKLLPVLDPSGDYVYMWLNTMVPVWYNIILVCRACFPD 60
QY 61 LQHGVLVAMLVLDYTSDDLTYLDMVVRFTHTGFLQGIILVNDKGRISRYRTWSPFLDLA 120
DB 61 LQHGVLVAMLVLDYTSDDLTYLDMVVRFTHTGFLQGIILVNDKGRISRYRTWSPFLDLA 120
QY 121 SLMPDVVVYVRLGPHPTLRNLRLAPRLFEAFDTEETRTAYVPAFRIAKMLYIFVVI 180
DB 121 SLMPDVVVYVRLGPHPTLRNLRLAPRLFEAFDTEETRTAYVPAFRIAKMLYIFVVI 180
QY 181 HNMSCLYFALSRYLGFGRDAMVYPPDAPGFERLRQYLYSFYSTLILTTVGDPPEPAR 240
DB 181 HNMSCLYFALSRYLGFGRDAMVYPPDAPGFERLRQYLYSFYSTLILTTVGDPPEPAR 240
QY 241 EEEYLFVWGDFLIIVMGFATIMGSMSSVYNNMTADAAPYPDHALVKKYMKLQHVNRKLE 300
DB 241 EEEYLFVWGDFLIIVMGFATIMGSMSSVYNNMTADAAPYPDHALVKKYMKLQHVNRKLE 300
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QY 301 RRVIDWYQHLOINKMTNEVALLOHLPERLRABVAVSHLSTLSRVQIFONCEASLLEBL 360
DB 301 RRVIDWYQHLOINKMTNEVALLOHLPERLRABVAVSHLSTLSRVQIFONCEASLLEBL 360
QY 361 VLKLPQYTPSPGEYVCRKGDIGQEWYIIRREGOLAVADGDITQYVVLGAGYFGEISITIN 420
DB 361 VLKLPQYTPSPGEYVCRKGDIGQEWYIIRREGOLAVADGDITQYVVLGAGYFGEISITIN 420
QY 421 IKGNSGNRRRTANISLGYSDFCLSKEDLRVLSSEYPOAQTIMEKREILKKXNKLDV 480
DB 421 IKGNSGNRRRTANISLGYSDFCLSKEDLRVLSSEYPOAQTIMEKREILKKXNKLDV 480
QY 481 NAAEIALQENTSRRLGDLQOQDDLOTKFARLILAESSALKYATIEELWOTRWP 540
DB 481 NAAEIALQENTSRRLGDLQOQDDLOTKFARLILAESSALKYATIEELWOTRWP 540
QY 541 MPEDIAEADDEGEPEGTSGKDEGRASQEGPGE 575
DB 541 MPEDIAEADDEGEPEGTSGKDEGRASQEGPGE 575
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RESULT 6
US-10-311-624-1
; Sequence 1, Application US/10311624
; Publication No. US20040127683A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: RAUMANN, Brigitte E.
; APPLICANT: Sanjwala, Madhu S.
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: Walla, Narinder K.
; TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
; FILE REFERENCE: SI-0141 PCT
; CURRENT APPLICATION NUMBER: US/10/311,624
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: 60/215,391
; PRIOR FILING DATE: 2000-06-29
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 6703242CD1
US-10-311-624-1
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Query Match          99.8%; Score 2984; DB 16; Length 575;
Best Local Similarity 99.8%; Pred. No. 4.8e-253;
Matches 574; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSODTKVKTSSPPAPSKARKLLPVLDPSGDYVYMWLNTMVPVWYNIILVCRACFPD 60
DB 1 MSODTKVKTSSPPAPSKARKLLPVLDPSGDYVYMWLNTMVPVWYNIILVCRACFPD 60
QY 61 LQHGVLVAMLVLDYTSDDLTYLDMVVRFTHTGFLQGIILVNDKGRISRYRTWSPFLDLA 120
DB 61 LQHGVLVAMLVLDYTSDDLTYLDMVVRFTHTGFLQGIILVNDKGRISRYRTWSPFLDLA 120
QY 121 SLMPDVVVYVRLGPHPTLRNLRLAPRLFEAFDTEETRTAYVPAFRIAKMLYIFVVI 180
DB 121 SLMPDVVVYVRLGPHPTLRNLRLAPRLFEAFDTEETRTAYVPAFRIAKMLYIFVVI 180
QY 181 HNMSCLYFALSRYLGFGRDAMVYPPDAPGFERLRQYLYSFYSTLILTTVGDPPEPAR 240
DB 181 HNMSCLYFALSRYLGFGRDAMVYPPDAPGFERLRQYLYSFYSTLILTTVGDPPEPAR 240
QY 241 EEEYLFVWGDFLIIVMGFATIMGSMSSVYNNMTADAAPYPDHALVKKYMKLQHVNRKLE 300
DB 241 EEEYLFVWGDFLIIVMGFATIMGSMSSVYNNMTADAAPYPDHALVKKYMKLQHVNRKLE 300
QY 301 RRVIDWYQHLOINKMTNEVALLOHLPERLRABVAVSHLSTLSRVQIFONCEASLLEBL 360
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Db 301 RRVIMYOHLOQINKKMTNEVALIQHLPERLRAEVAVSVHLSTLSRVQIFONCEASLLEL 360  
Qy 361 VLKLOPQYTSRPGYVCRKGDIGQEMYYIRREGOLAVVADGITYAVLAGLYGGEISII 420  
Db 361 VLKLOPQYTSRPGYVCRKGDIGQEMYYIRREGOLAVVADGITYAVLAGLYGGEISII 420  
Qy 421 IKGNMGNRRRTANIKSLGYSDFCLSKEDLREVLSEYPOQOTIMEKREILLKXNKLDV 480  
Db 421 IKGNMGNRRRTANIKSLGYSDFCLSKEDLREVLSEYPOQOTIMEKREILLKXNKLDV 480  
Qy 481 NAEAEIALQEAATESRLRGDQDDLDLQTKFARLLAELESSALKIAYRIERLEWOTREMP 540  
Db 481 NAEAEIALQEAATESRLRGDQDDLDLQTKFARLLAELESSALKIAYRIERLEWOTREMP 540  
Qy 541 MPEDLAADDEGEPEBEGTSKDEGRASQGGPPGPE 575  
Db 541 MPEDLAADDEGEPEBEGTSKDEGRASQGGPPGPE 575

## RESULT 7

US-09-842-758-28  
; Sequence 28, Application US/09842758  
; Publication No. US20030083244A1  
; GENERAL INFORMATION:  
; APPLICANT: Vernet, Corine A. M.  
; APPLICANT: Fernandes, Elma R.  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Shinkens, Richard A.  
; APPLICANT: Malyankar, Uriel M.  
; APPLICANT: Boldog, Ferenc L.  
; APPLICANT: Zernusen, Bryan D.  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Majumder, Kamud  
; APPLICANT: Tchernev, Velizar T.  
; APPLICANT: Padigarau, Muralidhara  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Gangolli, Beha A.  
; APPLICANT: Smithson, Glenda  
; APPLICANT: MacDougall, John R.  
; APPLICANT: Taupier, Raymond J.  
; APPLICANT: Groese, William M.  
; APPLICANT: Edward, Szekeres S.  
; APPLICANT: Alsbrook II, John P.  
; TITLE OF INVENTION: No. US20030083244A1 Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 15966-783  
; CURRENT APPLICATION NUMBER: US/09/842,758  
; PRIOR FILING DATE: 2001-04-25  
; PRIOR APPLICATION NUMBER: 60/200,158  
; PRIOR FILING DATE: 2000-04-26  
; PRIOR APPLICATION NUMBER: 60/200,613  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/200,780  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/201,006  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: 60/201,007  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: 60/201,236  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: 60/201,238  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: 60/201,186  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 60/201,474  
; PRIOR FILING DATE: 2000-05-03  
; PRIOR APPLICATION NUMBER: 60/201,508  
; PRIOR FILING DATE: 2000-05-03  
; PRIOR APPLICATION NUMBER: 60/220,591  
; PRIOR FILING DATE: 2000-07-25  
; PRIOR APPLICATION NUMBER: 60/232,678

; PRIOR FILING DATE: 2000-09-15  
; PRIOR APPLICATION NUMBER: 60/263,217  
; PRIOR FILING DATE: 2001-01-22  
; PRIOR APPLICATION NUMBER: 60/265,160  
; PRIOR FILING DATE: 2001-01-30  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 578  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-842-758-28

Query Match 98.9%; Score 2957.5; DB 10; Length 578;  
Best Local Similarity 99.5%; Pred. No. 1e-250;  
Matches 575; Conservative 0; Mismatches 0; Indels 3; Gaps 3;

Qy 1 MSQDTKVKTTSSPPAPSKA-RKLLPVLDPSGDYVWMLNTMVFVMTNLIILVCRACFP 59  
Db 1 MSQDTKVKTTSSPPAPSKARKLLPVLDPSGDYVWMLNTMVFVMTNLIILVCRACFP 60  
Qy 60 DLQHGVLVAVLVDTSDLVLLDMVVRFT-GLIEGILLVVDKGRISRYRTWSFFLD 118  
Db 61 DLQHGVLVAVLVDTSDLVLLDMVVRFTGGLIEGILLVVDKGRISRYRTWSFFLD 120  
Qy 119 LASLMPDVVYVRLGPHPTLRLNRLAPRLFEAFDTERETRTAYPNAFRLAKMLYIFV 178  
Db 121 LASLMPDVVYVRLGPHPTLRLNRLAPRLFEAFDTERETRTAYPNAFRLAKMLYIFV 180  
Qy 179 VIHNSCLYFALSRYLFGFGRDAVVPDPAQGFERLROLYSYFFSTLIITVGDTPP 238  
Db 181 VIHNSCLYFALSRYLFGFGRDAVVPDPAQGFERLROLYSYFFSTLIITVGDTPP 240  
Qy 239 ARREYLFVWGDFFLAVWGFATIMSSSVYNNMTAAPFDPBALVKKWKLVNVRK 298  
Db 241 ARREYLFVWGDFFLAVWGFATIMSSSVYNNMTAAPFDPBALVKKWKLVNVRK 300  
Qy 299 LERRVIDWYOHLOQINKKMTNEVALIQHLPERLRAEVAVSVHLSTLSRVQIFONCEASLLE 358  
Db 301 LERRVIDWYOHLOQINKKMTNEVALIQHLPERLRAEVAVSVHLSTLSRVQIFONCEASLLE 360  
Qy 359 ELVNLQPTYSRPGYVCRKGDIGQEMYYIRREGOLAVVADGITYAVLAGLYGGEISII 418  
Db 361 ELVNLQPTYSRPGYVCRKGDIGQEMYYIRREGOLAVVADGITYAVLAGLYGGEISII 420  
Qy 419 INIKGNMGNRRRTANIKSLGYSDFCLSKEDLREVLSEYPOQOTIMEKREILLKXNK 477  
Db 421 INIKGNMGNRRRTANIKSLGYSDFCLSKEDLREVLSEYPOQOTIMEKREILLKXNK 480  
Qy 478 LDVNAEAEIALQEAATESRLRGDQDDLDLQTKFARLLAELESSALKIAYRIERLEWOTR 537  
Db 481 LDVNAEAEIALQEAATESRLRGDQDDLDLQTKFARLLAELESSALKIAYRIERLEWOTR 540  
Qy 538 EWPMPEDLAADDEGEPEBEGTSKDEGRASQGGPPGPE 575  
Db 541 EWPMPEDLAADDEGEPEBEGTSKDEGRASQGGPPGPE 578

## RESULT 8

US-10-174-333-28  
; Sequence 28, Application US/10174333  
; Publication No. US20040029220A1  
; GENERAL INFORMATION:  
; APPLICANT: Vernet, Corine A. M.  
; APPLICANT: Fernandes, Elma R.  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Malyankar, Uriel M.  
; APPLICANT: Boldog, Ferenc L.  
; APPLICANT: Zernusen, Bryan D.  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Majumder, Kamud  
; APPLICANT: Tchernev, Velizar T.  
; APPLICANT: Padigarau, Muralidhara

```

APPLICANT: Paturajan, Meera
APPLICANT: Burgess, Catherine E.
APPLICANT: Gangoli, Seta A.
APPLICANT: Smithson, Glenda
APPLICANT: Raetelli, Luca
APPLICANT: MacDougall, John R.
APPLICANT: Taupier, Raymond J.
APPLICANT: Grosee, William M.
APPLICANT: Szekeres, Edward S.
APPLICANT: Alsobrook, John P.
APPLICANT: Anderson, David W.
APPLICANT: Guo, Xiaojia (Sasha)
APPLICANT: Li, Li
APPLICANT: Zhong, Mei
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-783 CIP1
CURRENT FILING DATE: US/10/174,333
PRIOR FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: 60/193,664
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 60/194,614
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: 60/195,063
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,066
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,067
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,068
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,069
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,070
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,510
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/219,855
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 186
SOFTWARE: CuiSeqLast version 0.1
SEQ ID NO 28
LENGTH: 578
TYPE: PRT
ORGANISM: Homo sapiens
US-10-174-333-28

```

```

Query Match          98.9%; Score 2957.5; DB 15; Length 578;
Best Local Similarity 99.5%; Pred. No. 1e-250;
Matches 575; Conservative 0; Mismatches 0; Indels 3; Gaps 3;

QY 1 MSODTKVKTSSPPAPSKA-RKLLPVLDPSGDYVYMWLNTMVPVWYNIILIVCRACFP 59
DB 1 MSODTKVKTSSPPAPSKARKKLPLVLDPSGDYVYMWLNTMVPVWYNIILIVCRACFP 60
QY 60 DLQGYLVAMLVLDYTSDLLYLDMVVRFHT-GFLEGGILVVDGRTSSRRVWTSFELD 118
DB 61 DLQGYLVAMLVLDYTSDLLYLDMVVRFHTGFLGQILVVDGRTSSRRVWTSFELD 120
QY 119 LASLMPDVTYVVRGLGPHPTPLRLNRLAPRLFEAFRTETRTAYPNAFRIAKMLYIFV 148
DB 121 LASLMPDVTYVVRGLGPHPTPLRLNRLAPRLFEAFRTETRTAYPNAFRIAKMLYIFV 180
QY 179 VIHNSCLYFALSYLGRDAMVYPPDPAOGFRLRQVLYSYFSTLITTVGDTPPP 238
DB 181 VIHNSCLYFALSYLGRDAMVYPPDPAOGFRLRQVLYSYFSTLITTVGDTPPP 240
QY 239 ARBEERYLFMGVDFLLAVMGFATIMGSSSVIYNNNTADAAFYPDHALVKKYMKLOHYNRK 238
DB 241 ARBEERYLFMGVDFLLAVMGFATIMGSSSVIYNNNTADAAFYPDHALVKKYMKLOHYNRK 300
QY 299 LERRVIDWYQHLOQINKKMTNEVALLOHLPERLRAEVAVSVHLSTLSRVQIFONCEASLLE 358

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DB 301 LERRVIDWYQHLOQINKKMTNEVALLOHLPERLRAEVAVSVHLSTLSRVQIFONCEASLLE 360
QY 359 ELVVKLOPQYSPGEYVCRKGDIGQEMYIIEGQAVVADGITOYAVLGAIFYGEISI 418
DB 361 ELVVKLOPQYSPGEYVCRKGDIGQEMYIIEGQAVVADGITOYAVLGAIFYGEISI 420
QY 419 INIK-GMNGRRNTANISLGSYDLFCLSKEDLREVTSEYQAOITMEKREILLKXNK 477
DB 421 INIKGMNGRRNTANISLGSYDLFCLSKEDLREVTSEYQAOITMEKREILLKXNK 480
QY 478 LDVNAEAEIALQEXTESRLGLDQDDLOTKFARILAEISSALKIATVIERLEWOTR 537
DB 481 LDVNAEAEIALQEXTESRLGLDQDDLOTKFARILAEISSALKIATVIERLEWOTR 540
QY 538 EWPMPEDIAEADDEGEPEEGTSKDEGRASQEGCPGE 575
DB 541 EWPMPEDIAEADDEGEPEEGTSKDEGRASQEGCPGE 578

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RESULT 9
US-09-735-932-4
Sequence 4, Application US/09735932
Patent No. US20020037548A1
GENERAL INFORMATION:
APPLICANT: GUEGLER, Karl et al
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUM AN TRANSPORTER PROTEINS,
FILE REFERENCE: CL000663
CURRENT FILING DATE: US/09/735,932
NUMBER OF SEQ ID NOS: 2000-12-14
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 575
TYPE: PRT
ORGANISM: Rattus norvegicus
US-09-735-932-4

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Query Match          94.0%; Score 2811; DB 9; Length 575;
Best Local Similarity 93.4%; Pred. No. 7.7e-238;
Matches 537; Conservative 16; Mismatches 22; Indels 0; Gaps 0;

QY 1 MSODTKVKTSSPPAPSKARKKLPLVLDPSGDYVYMWLNTMVPVWYNIILIVCRACFP 60
DB 1 MSODTKVKTSSPPAPSKARKKLPLVLDPSGDYVYMWLNTMVPVWYNIILIVCRACFP 60
QY 61 LQHSYLVAMLVLDYTSDLLYLDMVVRFHTGFLGQILVVDGRTSSRRVWTSFELDIA 120
DB 61 LQHSYLVAMLVLDYTSDLLYLDMVVRFHTGFLGQILVVDGRTSSRRVWTSFELDIA 120
QY 121 SLMPDVTYVVRGLGPHPTPLRLNRLAPRLFEAFRTETRTAYPNAFRIAKMLYIFVYI 180
DB 121 SLMPDVTYVVRGLGPHPTPLRLNRLAPRLFEAFRTETRTAYPNAFRIAKMLYIFVYI 180
QY 181 HNSCLYFALSYLGRDAMVYPPDPAOGFRLRQVLYSYFSTLITTVGDTPPP 240
DB 181 HNSCLYFALSYLGRDAMVYPPDPAOGFRLRQVLYSYFSTLITTVGDTPPP 240
QY 241 EBEERYLFMGVDFLLAVMGFATIMGSSSVIYNNNTADAAFYPDHALVKKYMKLOHYNRKLE 300
DB 241 EBEERYLFMGVDFLLAVMGFATIMGSSSVIYNNNTADAAFYPDHALVKKYMKLOHYNRKLE 300
QY 301 RRVVIDWYQHLOQINKKMTNEVALLOHLPERLRAEVAVSVHLSTLSRVQIFONCEASLLEEL 360
DB 301 RRVVIDWYQHLOQINKKMTNEVALLOHLPERLRAEVAVSVHLSTLSRVQIFONCEASLLEEL 360
QY 361 VIKLOPQYSPGEYVCRKGDIGQEMYIIEGQAVVADGITOYAVLGAIFYGEISIIN 420
DB 361 VIKLOPQYSPGEYVCRKGDIGQEMYIIEGQAVVADGITOYAVLGAIFYGEISIIN 420
QY 421 IKGNNGRRNTANISLGSYDLFCLSKEDLREVTSEYQAOITMEKREILLKXNKIDV 480

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Db 421 IKGNNSGNRRNTANIKSLGYSDLFCLSKEDLREVLSEYPOQAAMEKREILLKNKLDV 480  
QY 481 NAAEAIALQEAATESRLGLDQDLDTQKFARLAELESSALKIAYRIERLEWQTRMP 540  
Db 481 NAAEAIALQEAATESRLGLDQDLDTQKFARLAELESSALKIAYRIERLEWQTRMP 540  
QY 541 MPEDLAEDDEGEPEEGTSGKDEGRASQEGPPGPE 575  
Db 541 MPEDWGEADDEAEPEEGTSGKDEGRAGAGAPSGIE 575

RESULT 10  
US-09-927-267-16  
Sequence 16, Application US/09927267  
Publication No. US20020182691A1  
GENERAL INFORMATION:  
APPLICANT: Crech, Christopher D.  
APPLICANT: Jegla, Timothy J.  
APPLICANT: ICAGEN, Inc.  
TITLE OF INVENTION: CNG2B: A No. US20020182691A1el Human Cyclic Nucleotide-Gated Ion  
TITLE OF INVENTION: Channel  
FILE REFERENCE: 018512-006510US  
CURRENT APPLICATION NUMBER: US/09/927,267  
CURRENT FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: US 60/226,253  
PRIOR FILING DATE: 2000-08-17  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 16  
LENGTH: 575  
TYPE: PRT  
ORGANISM: Rattus norvegicus  
FEATURE:  
OTHER INFORMATION: rat cyclic nucleotide gated cation channel OCN2  
US-09-927-267-16

Query Match 94.0%; Score 2811; DB 9; Length 575;  
Best Local Similarity 93.4%; Pred. No. 7,7e-238;  
Matches 537; Conservative 16; Mismatches 22; Indels 0; Gaps 0;

QY 1 MSQDTRKVTSSPPAPSAKRLPVLDPSGDIYVWMLTWFPVWYNIILVCRACFPD 60  
Db 1 MSQDGVKTTSTPAPPAKRLPVLDPSGDIYVWMLTWFPVWYNIILVCRACFPD 60  
QY 61 LOHGVLAIVLVLDYSDLLYLDMVVRFTGFLGEGIIIVNDGRISRRVYRWSFLDIA 120  
Db 61 LOHGVLAIVLVLDYSDLLYLDMVVRFTGFLGEGIIIVNDGRISRRVYRWSFLDIA 120  
QY 121 SIAPTDVVVVRIGPPTPLRLNRPFLAPFLFAFDRTETRTAYVPAFRIAKMLYFVVI 180  
Db 121 SIAPTDVVVVRIGPPTPLRLNRPFLAPFLFAFDRTETRTAYVPAFRIAKMLYFVVI 180  
QY 121 SIAPTDVVVVRIGPPTPLRLNRPFLAPFLFAFDRTETRTAYVPAFRIAKMLYFVVI 180  
Db 121 SIAPTDVVVVRIGPPTPLRLNRPFLAPFLFAFDRTETRTAYVPAFRIAKMLYFVVI 180  
QY 181 HNSNCLYFALSYLFGGRDAMYPPDAQGFERLRQYLYSFYSTLLITTVGDTPPPAR 240  
Db 181 HNSNCLYFALSYLFGGRDAMYPPDAQGFERLRQYLYSFYSTLLITTVGDTPPPAR 240  
QY 181 HNSNCLYFALSYLFGGRDAMYPPDAQGFERLRQYLYSFYSTLLITTVGDTPPPAR 240  
Db 181 HNSNCLYFALSYLFGGRDAMYPPDAQGFERLRQYLYSFYSTLLITTVGDTPPPAR 240  
QY 241 EEEYLFMVGDDELLAWGFAITMGSMSSVYNNMTADAAYPPHAIYKTKMLQHVNRKE 300  
Db 241 EEEYLFMVGDDELLAWGFAITMGSMSSVYNNMTADAAYPPHAIYKTKMLQHVNRKE 300  
QY 241 EEEYLFMVGDDELLAWGFAITMGSMSSVYNNMTADAAYPPHAIYKTKMLQHVNRKE 300  
Db 241 EEEYLFMVGDDELLAWGFAITMGSMSSVYNNMTADAAYPPHAIYKTKMLQHVNRKE 300  
QY 301 RRVIMVYQHLQINKKTNVAILQHLPERLRAEVAIVSHTLSRQVIFONCEASLLEEL 360  
Db 301 RRVIMVYQHLQINKKTNVAILQHLPERLRAEVAIVSHTLSRQVIFONCEASLLEEL 360  
QY 361 VLKLPQTVSPGEYVCRKDDIGQEMYIIRGQLAVVADDTQYAVLAGLYFGEISIN 420  
Db 361 VLKLPQTVSPGEYVCRKDDIGQEMYIIRGQLAVVADDTQYAVLAGLYFGEISIN 420  
QY 421 IKGNNSGNRRNTANIKSLGYSDLFCLSKEDLREVLSEYPOQAAMEKREILLKNKLDV 480  
Db 421 IKGNNSGNRRNTANIKSLGYSDLFCLSKEDLREVLSEYPOQAAMEKREILLKNKLDV 480  
QY 481 NAAEAIALQEAATESRLGLDQDLDTQKFARLAELESSALKIAYRIERLEWQTRMP 540  
Db 481 NAAEAIALQEAATESRLGLDQDLDTQKFARLAELESSALKIAYRIERLEWQTRMP 540

Db 481 NAAEAIALQEAATESRLGLDQDLDTQKFARLAELESSALKIAYRIERLEWQTRMP 540  
QY 541 MPEDLAEDDEGEPEEGTSGKDEGRASQEGPPGPE 575  
Db 541 MPEDWGEADDEAEPEEGTSGKDEGRAGAGAPSGIE 575

RESULT 11  
US-09-842-758-74  
Sequence 74, Application US/09842758  
Publication No. US20030083244A1  
GENERAL INFORMATION:  
APPLICANT: Vernet, Corine A. M.  
APPLICANT: Fernandes, Elma R.  
APPLICANT: Gerlach, Valerie  
APPLICANT: Shinkets, Richard A.  
APPLICANT: Malyankar, Uriel M.  
APPLICANT: Boldog, Ferenc L.  
APPLICANT: Zernusen, Bryan D.  
APPLICANT: Spytek, Kimberly A.  
APPLICANT: Majumder, Kunud  
APPLICANT: Tchernev, Vellizar T.  
APPLICANT: Padigaru, Muralidhara  
APPLICANT: Patturajan, Meera  
APPLICANT: Burgess, Catherine E.  
APPLICANT: Gangoli, Esba A.  
APPLICANT: Smithson, Glenda  
APPLICANT: Rastelli, Luca  
APPLICANT: MacDougall, John R.  
APPLICANT: Taupier, Raymond J.  
APPLICANT: Grosse, William M.  
APPLICANT: Edward, Szekeres S.  
APPLICANT: Alsbrook II, John P.  
TITLE OF INVENTION: No. US20030083244A1el Proteins and Nucleic Acids Encoding Same  
FILE REFERENCE: 15966-783  
CURRENT APPLICATION NUMBER: US/09/842,758  
CURRENT FILING DATE: 2001-04-25  
PRIOR APPLICATION NUMBER: 60/200,158  
PRIOR FILING DATE: 2000-04-26  
PRIOR APPLICATION NUMBER: 60/200,613  
PRIOR FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: 60/200,780  
PRIOR FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: 60/201,006  
PRIOR FILING DATE: 2000-05-01  
PRIOR APPLICATION NUMBER: 60/201,007  
PRIOR FILING DATE: 2000-05-01  
PRIOR APPLICATION NUMBER: 60/201,236  
PRIOR FILING DATE: 2000-05-01  
PRIOR APPLICATION NUMBER: 60/201,238  
PRIOR FILING DATE: 2000-05-01  
PRIOR APPLICATION NUMBER: 60/201,186  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 60/201,474  
PRIOR FILING DATE: 2000-05-03  
PRIOR APPLICATION NUMBER: 60/201,508  
PRIOR FILING DATE: 2000-05-03  
PRIOR APPLICATION NUMBER: 60/220,591  
PRIOR FILING DATE: 2000-07-25  
PRIOR APPLICATION NUMBER: 60/232,678  
PRIOR FILING DATE: 2000-09-15  
PRIOR APPLICATION NUMBER: 60/263,217  
PRIOR FILING DATE: 2001-01-22  
PRIOR APPLICATION NUMBER: 60/265,160  
PRIOR FILING DATE: 2001-01-30  
NUMBER OF SEQ ID NOS: 113  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 74  
LENGTH: 575  
TYPE: PRT  
ORGANISM: Rattus norvegicus  
US-09-842-758-74

```

Query Match      94.0%; Score 2811; DB 10; Length 575;
Best Local Similarity 93.4%; Pred. No. 7,7e-238;
Matches 537; Conservative 16; Mismatches 22; Indels 0; Gaps 0;

QY 1 MSODTKKTTSESPAPSKARKLLPVLDPSGDYYWMLNTMPVPMYMLIIVCRACFPD 60
DB 1 MSODGKVKTTSETPPATKARKWLPVLDPSGDYYWMLNTMPVPMYMLIIVCRACFPD 60
QY 61 LOHGYLVAMVLVLYTSDLYLIDMVVRPHTGFLFEOGILVVDKGRISRYRTWSFLDLA 120
DB 61 LOHSYLVAMFVLDYTDLYLIDIGVRFHTGFLFEOGILVVDKGRISRYRTWSFLDLA 120
QY 121 SLMPDTVVYVRLGPHPTPTLRNLNPLRPAFLFEAFDRTETRTAYPAFRIAKMLYIFVYI 180
DB 121 SLVPTDAAAYVQLGPHIPTLRNLNPLRPAFLFEAFDRTETRTAYPAFRIAKMLYIFVYI 180
QY 181 HNSCLYFALSRVLGGRDAWVYPPDAOGFEBRLRQYLYSFFSTLIITTVGDTPEPPAR 240
DB 181 HNSCLYFALSRVLGGRDAWVYPPDAOGFEBRLRQYLYSFFSTLIITTVGDTPEPPAR 240
QY 241 EEEYLFMVGDPLLAVMGFATINGSMSVLYNNMTADAAPYPPHALVKYMKLOHVNKRL 300
DB 241 EEEYLFMVGDPLLAVMGFATINGSMSVLYNNMTADAAPYPPHALVKYMKLOHVNKRL 300
QY 301 RRVIVMYOHLQINKKMTNEVALLOHLPERLRAEVAVSVHLSLRSVQIFONCEASILEEL 360
DB 301 RRVIVMYOHLQINKKMTNEVALLOHLPERLRAEVAVSVHLSLRSVQIFONCEASILEEL 360
QY 361 VKLQOPQYSPGEYVCRKDGIGOEYITREGOLAVVADGIGQYAVLGAGLFGEISITIN 420
DB 361 VKLQOPQYSPGEYVCRKDGIGOEYITREGOLAVVADGIGQYAVLGAGLFGEISITIN 420
QY 421 IKGNSGNRRNTANIKSLGYSDLFCLSKEDLREVLSEYPOAQTIMEKGREILLKNNKLDV 480
DB 421 IKGNSGNRRNTANIKSLGYSDLFCLSKEDLREVLSEYPOAQTIMEKGREILLKNNKLDV 480
QY 481 NAEAEIALOEAETSERLGLDOQLDQTKPARLAEISSALKTAYIERLEWOTREMP 540
DB 481 NAEAEIALOEAETSERLGLDOQLDQTKPARLAEISSALKTAYIERLEWOTREMP 540
QY 541 MPEDLAADDEGEPEEGTSKDEGRASOEGPPGPE 575
DB 541 MPEDWGEADDEAEPEEGTSKDEGRASOEGPPGPE 575

RESULT 12
US-10-174-333-74
; Sequence 74, Application US/10174333
; Publication No. US20040029220A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Majumder, Kunud
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Paturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Gangolli, Esna A.
; APPLICANT: Smithson, Glenda
; APPLICANT: Rastelli, Luca
; APPLICANT: MacDougall, John R.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Grose, William M.
; APPLICANT: Szekeres, Edward S.
; APPLICANT: Alebrook, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Guo, Xiaojia (Sasha)

```

```

; APPLICANT: Li, Li
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-783 CIP1
; CURRENT APPLICATION NUMBER: US/10/174,333
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 60/193,664
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 60/194,614
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 60/195,063
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,066
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,067
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,068
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,069
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,070
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,510
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/219,855
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: Cursedq1st version 0.1
; SEQ ID NO 74
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; US-10-174-333-74

Query Match      94.0%; Score 2811; DB 15; Length 575;
Best Local Similarity 93.4%; Pred. No. 7,7e-238;
Matches 537; Conservative 16; Mismatches 22; Indels 0; Gaps 0;

QY 1 MSODTKKTTSESPAPSKARKLLPVLDPSGDYYWMLNTMPVPMYMLIIVCRACFPD 60
DB 1 MSODGKVKTTSETPPATKARKWLPVLDPSGDYYWMLNTMPVPMYMLIIVCRACFPD 60
QY 61 LOHGYLVAMVLVLYTSDLYLIDMVVRPHTGFLFEOGILVVDKGRISRYRTWSFLDLA 120
DB 61 LOHSYLVAMFVLDYTDLYLIDIGVRFHTGFLFEOGILVVDKGRISRYRTWSFLDLA 120
QY 121 SLMPDTVVYVRLGPHPTPTLRNLNPLRPAFLFEAFDRTETRTAYPAFRIAKMLYIFVYI 180
DB 121 SLVPTDAAAYVQLGPHIPTLRNLNPLRPAFLFEAFDRTETRTAYPAFRIAKMLYIFVYI 180
QY 181 HNSCLYFALSRVLGGRDAWVYPPDAOGFEBRLRQYLYSFFSTLIITTVGDTPEPPAR 240
DB 181 HNSCLYFALSRVLGGRDAWVYPPDAOGFEBRLRQYLYSFFSTLIITTVGDTPEPPAR 240
QY 241 EEEYLFMVGDPLLAVMGFATINGSMSVLYNNMTADAAPYPPHALVKYMKLOHVNKRL 300
DB 241 EEEYLFMVGDPLLAVMGFATINGSMSVLYNNMTADAAPYPPHALVKYMKLOHVNKRL 300
QY 301 RRVIVMYOHLQINKKMTNEVALLOHLPERLRAEVAVSVHLSLRSVQIFONCEASILEEL 360
DB 301 RRVIVMYOHLQINKKMTNEVALLOHLPERLRAEVAVSVHLSLRSVQIFONCEASILEEL 360
QY 361 VKLQOPQYSPGEYVCRKDGIGOEYITREGOLAVVADGIGQYAVLGAGLFGEISITIN 420
DB 361 VKLQOPQYSPGEYVCRKDGIGOEYITREGOLAVVADGIGQYAVLGAGLFGEISITIN 420
QY 421 IKGNSGNRRNTANIKSLGYSDLFCLSKEDLREVLSEYPOAQTIMEKGREILLKNNKLDV 480
DB 421 IKGNSGNRRNTANIKSLGYSDLFCLSKEDLREVLSEYPOAQTIMEKGREILLKNNKLDV 480
QY 481 NAEAEIALOEAETSERLGLDOQLDQTKPARLAEISSALKTAYIERLEWOTREMP 540
DB 481 NAEAEIALOEAETSERLGLDOQLDQTKPARLAEISSALKTAYIERLEWOTREMP 540

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Db 481 NAAEALAEATSRRLKGLDQDLDTKFAARLLAELESSALKIAYRIERLEWQREMP 540  
QY 541 MEDLAADDEGEPEEGTSGDEGRASQEGPPGPE 575  
Db 541 MEDMGADDEGEPEEGTSGDEGRASQEGPPGPE 575

RESULT 13  
US-10-207-951-4  
; Sequence 4, Application US/10207951  
; Publication No. US20030013156A1  
; GENERAL INFORMATION:  
; APPLICANT: KARL GUEGLER et al.  
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS  
; TITLE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: CLO00663CON  
; CURRENT APPLICATION NUMBER: US/10/207,951  
; CURRENT FILING DATE: 2002-07-31  
; PRIOR APPLICATION NUMBER: 09/735,932  
; PRIOR FILING DATE: 2000-12-14  
; PRIOR APPLICATION NUMBER: 60/211,223  
; PRIOR FILING DATE: 2000-06-13  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO: 4  
; LENGTH: 1704  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-10-207-951-4

Query Match 80.1%; Score 2394; DB 14; Length 1704;  
Best Local Similarity 37.1%; Pred No. 1.8e-200;  
Matches 567; Conservative 5; Mismatches 3; Indels 952; Gaps 9;

QY 1 MSQDTKVTTESSPPAPSKARKLLPYLDSGDYYWMLNTWFPVWYNLLILVCRACFPD 60  
Db 117 MSQDKVKTTSTPAPTKARKMLPYLDSGDYYWMLNTWFPVWYNLLILVCRACFPD 176  
QY 61 -LQHGIVAMLVLDYTSDDLILDMVVRPHGTGFLBQGLIVVDKGRSSRYVWTSGFLDL 119  
Db 177 QLOHGIVAMLVLDYTSDDLILDMVVRPHGTGFLBQGLIVVDKGRSSRYVWTSGFLDL 236  
QY 120 A----- 120  
Db 237 ALQHTLVAMVLDYTSDDLILDMVVRPHGTGFLBQGLIVVDKGRSSRYVWTSGFLDLASLQHSY 296  
QY 121 -----SLMP 124  
Db 297 LVAMFVLDYTSDDLILDMVVRPHGTGFLBQGLIVVDKGRSSRYVWTSGFLDLASLMP 356  
QY 135 TDVVVVRGLGPHPTLRLNRLFLRPAFLFEAFDRTETRTAYPNAFRIAKMLYIFVVI 180  
Db 357 TDVVVVRGLGPHPTLRLNRLFLRPAFLFEAFDRTETRTAYPNAFRIAKMLYIFVVISLPT 416  
QY 181 ----- 180  
Db 417 DVLGPHPTLRLNRLFLRPAFLFEAFDRTETRTAYPNAFRIAKMLYIFVVISLPTDAY 476  
QY 181 -----HMNSCLYF 188  
Db 477 VQLGPHPTLRLNRLFLRPAFLFEAFDRTETRTAYPNAFRIAKMLYIFVVIQHMNSCLYF 536  
QY 189 ALSRYLGFGRDAMVYDDPAQPGFERLRQYLYSFYSTLILTTVGDTPPRSHNSCLYFA 240  
Db 537 ALSRYLGFGRDAMVYDDPAQPGFERLRQYLYSFYSTLILTTVGDTPPRSHNSCLYF 596  
QY 241 ----- 240  
Db 597 ALSRYLGFGRDAMVYDDPAQPGFERLRQYLYSFYSTLILTTVGDTPPRSHNSCLYFA 656  
QY 241 -----EEEYLFMV 248

Db 657 LSRYLGFGRDAMVYDDPAQPGFERLRQYLYSFYSTLILTTVGDTPPRSHNSCLYFA 716  
QY 249 GDFLLAVMGFATIMGSMSSVIYNNMTADAAFYPDHALVKYMKLOHVNLESEEEYLFMV 300  
Db 717 GDFLLAVMGFATIMGSMSSVIYNNMTADAAFYPDHALVKYMKLOHVNRLKEEYLFMV 776  
QY 301 ----- 300  
Db 777 GDFLLAVMGFATIMGSMSSVIYNNMTADAAFYPDHALVKYMKLOHVNLESEEEYLFMV 836  
QY 301 ----- 300  
Db 837 DFLAVMGFATIMGSMSSVIYNNMTADAAFYPDHALVKYMKLOHVNRLKEEYLFMV 896  
QY 301 ----- 300  
Db 897 HLQINKKMSNEVALIQHLPERLRAEVAVSHLSTLSRVQIFQNCESALLEELRVIDWYQ 956  
QY 301 -----RVIDWYQ 308  
Db 957 HLQINKKMSNEVALIQHLPERLRAEVAVSHLSTLSRVQIFQNCESALLEELRVIDWYQ 1016  
QY 309 HLQINKKMSNEVALIQHLPERLRAEVAVSHLSTLSRVQIFQNCESALLEELRVIDWYQ 367  
Db 1017 HLQINKKMSNEVALIQHLPERLRAEVAVSHLSTLSRVQIFQNCESALLEELRVIDWYQ 1076  
QY 368 TYPGEYVCRKGDIGQEMYIIRREGQLAVVADGITOYAVLAGLYFGESIIINVLKLPQ 420  
Db 1077 TYPGEYVCRKGDIGQEMYIIRREGQLAVVADGITOYAVLAGLYFGESIIINVLKLPQ 1136  
QY 421 ----- 420  
Db 1137 TYPGEYVCRKGDIGQEMYIIRREGQLAVVADGITOYAVLAGLYFGESIIINVLKLPQ 1196  
QY 421 ----- 420  
Db 1197 YSPGEYVCRKGDIGQEMYIIRREGQLAVVADGITOYAVLAGLYFGESIIINVLKLPQ 1256  
QY 421 ----- 420  
Db 1257 NRRTNINISLGSDFCLSKEDLREVLSYPOAQIMEKGREILLKMSKLDVIGKNSG 1316  
QY 421 -----IKNSGNR 430  
Db 1317 NRRTNINISLGSDFCLSKEDLREVLSYPOAQIMEKGREILLKMSKLDVIGKNSGNR 1376  
QY 431 TANIKSLGSDFCLSKEDLREVLSYPOAQIMEKGREILLKMSKLDVIGKNSGNR 1489  
Db 1377 TANIKSLGSDFCLSKEDLREVLSYPOAQIMEKGREILLKMSKLDVIGKNSGNR 1436  
QY 490 QEATESRLKGLDQDLDTKFAARLLAELESSALKIAYRIERLEWQREMP 540  
Db 1437 QEATESRLKGLDQDLDTKFAARLLAELESSALKIAYRIERLEWQREMP 1496  
QY 541 ----- 540  
Db 1497 QEATESRLKGLDQDLDTKFAARLLAELESSALKIAYRIERLEWQREMP 1556  
QY 541 -----MEDLA 548  
Db 1557 QEATESRLKGLDQDLDTKFAARLLAELESSALKIAYRIERLEWQREMP 1616  
QY 549 DDEGEPEEGTSGDEGRASQEGPPGPE 575  
Db 1617 DDEGEPEEGTSGDEGRASQEGPPGPE 1643

RESULT 14  
US-10-029-677-16  
; Sequence 16, Application US/10029677  
; Publication No. US20030096249A1  
; GENERAL INFORMATION:  
; APPLICANT: Westphal, Ryan S.



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 9, 2005, 20:48:30 : Search time 90 Seconds  
(without alignments)  
2291.882 Million cell updates/sec

Title: US-09-927-267-1

Perfect score: 2989  
Sequence: 1 MSQPTKVKVTESSPPAPSKA.....ECTSKDEGRASQSGPPPE 575

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

1: geneseqp1980s:\*\n2: geneseqp1990s:\*\n3: geneseqp2000s:\*\n4: geneseqp2001s:\*\n5: geneseqp2002s:\*\n6: geneseqp2003as:\*\n7: geneseqp2003bs:\*\n8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2989	100.0	575	5	ABP69252 Human pol
2	2989	100.0	575	5	AAE20959 Human tra
3	2989	100.0	575	5	ABR07725 Human tra
4	2989	100.0	575	6	ABU09091 Human tra
5	2989	100.0	575	6	ABP55141 Human tra
6	2989	100.0	575	6	ADH11623 Human tra
7	2984	99.8	575	5	AAO14138 Human tra
8	2984	99.8	575	5	AAW47673 Human tra
9	2984	99.8	575	5	ADJ87678 G-coupled
10	2982	99.8	575	6	ABU09778 Human tra
11	2957.5	98.9	578	5	AAW47672 MOLA pr
12	2957.5	98.9	578	7	ADJ87676 G-coupled
13	2957.5	98.9	578	8	ADN38409 Novel hum
14	2892	96.8	575	8	ADN38411 Novel hum
15	2889	96.7	568	6	ABP55142 Human tra
16	2384	80.1	1704	6	ABU09092 Rat trans
17	1568	52.5	663	5	AAE79527 Cow HBMC
18	1568	52.4	663	6	ABG74912 Bovine CN
19	1563	52.3	664	7	ADP56501 Modified
20	1563	52.3	663	6	ABG74914 Bovine CN
21	1562	52.3	663	6	ABG74913 Bovine CN
22	1562	52.3	732	5	AAE79526 Rabbit HB
23	1558	52.1	664	5	AAE79529 Rat HBMC
24	1558	52.1	664	6	AAE37219 Rat CNG c
25	1558	52.1	664	7	ADP56504 Rat olfac

26	1554	52.0	634	7	ADP56503 Modified
27	1554	52.0	664	6	AAE37221 Rat CNG c
28	1554	52.0	664	7	ADP56502 Modified
29	1553	52.0	664	6	AAE37224 Rat CNG c
30	1553	52.0	664	6	AAE37223 Rat CNG c
31	1551.5	51.9	664	5	AAE15987 Human CNG
32	1549.5	51.8	664	7	AAE38591 Human CNG
33	1549	51.8	664	6	AAE37220 Rat CNG c
34	1547	51.8	664	6	AAE79528 Mouse HBM
35	1545	51.7	664	6	AAE37222 Rat CNG c
36	1538.5	51.5	686	7	ADD48640 Human Pro
37	1535	51.4	664	4	AAE04894 Human tra
38	1535	51.4	664	5	ABE78066 Amino aci
39	1535	51.4	664	6	ABG72530 Novel hum
40	1535	51.4	664	6	ABG72529 Novel hum
41	1535	51.4	664	6	ABU12049 Human NOV
42	1535	51.4	664	6	ABP98475 Amino aci
43	1532	51.3	690	5	AAE15988 Human CNG
44	1532	51.3	664	5	AAE79525 Variant H
45	1532	51.3	683	7	ADD48638 Rat Prote

## ALIGNMENTS

RESULT 1	ABP69252	standard: protein; 575 AA.
ID	ABP69252	
XX	ABP69252;	
AC	ABP69252;	
XX	20-JAN-2003	(first entry)
DT	20-JAN-2003	
XX	Human polypeptide SEQ ID NO 1299.	
DE	Human polypeptide SEQ ID NO 1299.	
XX	Human; genome mapping; gene therapy; food supplement; virus; fungus;	
KW	cell-proliferative disorder; neurodegenerative disease; bacterial;	
KW	Parkinson's disease; Alzheimer's disease; autoimmune disease;	
KW	multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;	
KW	arthritis; cytosolic; immunomodulator; nocotropic; neuroprotective;	
KW	antiparkinsonian; antidiabetic; immunosuppressive; dermatological;	
KW	haemostatic; vulnery; fungicide; antibacterial; virucide; protozoacide;	
KW	antiarthritic.	
XX		
OS	Homo sapiens.	
PN	WO200270539-A2.	
XX		
PD	12-SEP-2002.	
XX		
PF	05-MAR-2002; 2002MO-US005095.	
XX		
PR	05-MAR-2001; 2001US-00799451.	
XX		
XX	(HYSE-) HYSEQ INC.	
XX	Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QH, Ren F;	
PI	Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;	
PI	Wehman T, Wang J, Wang D, Drmanac RT;	
DR	WPI; 2002-759812/82.	
XX	N-PSDB; ABZ11469.	
PT	New polynucleotides comprising sequences assembled from expressed	
PT	sequence tags (ESTs), useful for creating cell-proliferative,	
PT	neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet	
PT	or coagulation disorders.	
XX		
PS	Claim 9; SEQ ID NO 1299; 1012pp + Sequence Listing: English.	
CC	The invention relates to an isolated polynucleotide (I) comprising a	
CC	nucleotide sequence selected from any of 948 sequences (ABZ11119-	
CC	ABZ12066) or their mature protein coding portion, active domain coding	

	--sequences
Best Local Similarity	100.0%;
Matches	575

Index	Sequence	Indels	Gaps
1	MSGDTKVKITTESSPPASRKRTIPLVLPDSGDYYWMLNMTVEPVYNT	0	0

121 SLMPDVVVRLGPHPTPT .....LEQSLVNDKGRISRYVRTWSFFLLDA 120

180  
181 HNNSCLYFALSRYPGFCO ||||| LUF EAFDRETETRYAPNPAFIKIMLYIFVI 180

[illegible]

421 IKGNMGNMPP... 360

480  
481 NAAEALOEATRESPTDLOOTKPARLLEBESSATK  
480

LEGISKDEGRASQEGPPGPE 575

UL-2002 (First entry)

protein related cyclic nucleotide-gated ion channel; disease; gene therapy; transfection



Key	Location/Qualifiers
PT	40, 60
FT	
mm	

Region	Protein kinase C phosphorylation site
177-197	
197-217	

Modified-site  
region  
/note= "Casein kinase II phosphoryl  
256..276  
/label= Helix

Misc-difference phosphorylation site" /note="cAMP- and cGMP-dependent protein kinase 317

375. .391  
/note="Casein kinase II phosphorylation site"  
407

423. .436 Cysteoylation site  
/note="Cyclic nucleotide-binding site"  
423. .428

	/note= "N-myristoylation site"	-myristoylated"	432
c-difference	432		
ified-site	/note- "		

476	Casein kinase II phosphorylation site"
559	/note= "Encoded by ..."

539. .562 Casein kinase C phosphorylation site" /note="Casein kinase IT"

000; 2000US-0211223P.

Ketchum KA, Di Franco



XX MPI; 2002-315109/35.  
 DR N-PSDB; AAD33869.  
 XX Nucleic acids encoding cyclic nucleotide-gated ion channel subfamily  
 PT transporter proteins (Tpe), useful in prevention, diagnosis and treatment  
 PT of TP-related diseases.  
 XX  
 PS Claim 1; Fig 2; 45pp; English.  
 XX  
 CC The invention relates to nucleic acid sequences that encode protein  
 CC molecules which are members of the transporter family of proteins and are  
 CC related to the cyclic nucleotide-gated ion channel subfamily. The  
 CC transporter protein DNA may be used in the prevention, diagnosis and  
 CC treatment of diseases associated with inappropriate transporter protein  
 CC expression. Transporter protein and its DNA are used to treat disorders  
 CC associated with decreased transporter protein expression by rectifying  
 CC mutations or deletions in a patient's genome that affect the activity of  
 CC the transporter proteins by expressing inactive proteins or to supplement  
 CC the patients own production of them. Transporter protein DNA and its  
 CC complementary sequences may also be used in gene therapy and as DNA  
 CC probes in diagnostic assays and to detect and quantitate the presence of  
 CC similar nucleic acids in samples, and therefore which patients may be in  
 CC need of restorative therapy. They may also be used in the production of  
 CC transgenic animals in which transporter protein expression and activity  
 CC may be studied. Transporter protein is useful in protein therapy and in  
 CC the production of vaccines. The present sequence is human transporter  
 CC protein. Human transporter protein gene is located on chromosome 11  
 XX  
 XX Sequence 575 AA;  
 XX

Query Match 100.0%; Score 2989; DB 5; Length 575;  
 Best Local Similarity 100.0%; Pred. No. 8.7e-278;  
 Matches 575; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSODTKVKTSSPPAPSKARKLLPVLDPSSGDIYYWMLNTWFPVWYNIILIVCRACFPD 60  
 DB 1 MSODTKVKTSSPPAPSKARKLLPVLDPSSGDIYYWMLNTWFPVWYNIILIVCRACFPD 60  
 QY 61 LQHGVLVAMLVLDYSDLLYLDMVVRFRHTGFLBEGILVVDKGRISRRVYRTMSFFLDA 120  
 DB 61 LQHGVLVAMLVLDYSDLLYLDMVVRFRHTGFLBEGILVVDKGRISRRVYRTMSFFLDA 120  
 QY 121 SLMPDQVYVVRGPHPTPLRLRFLAPRLFEAFDSTETRTAYPNAFRIAKMLYIFVVI 180  
 DB 121 SLMPDQVYVVRGPHPTPLRLRFLAPRLFEAFDSTETRTAYPNAFRIAKMLYIFVVI 180  
 QY 181 HNSCLYFALSRYLGFGRDAMVYPDPAQGFELRLRQVLYSPFSTLILTTVGDTPPPAR 240  
 DB 181 HNSCLYFALSRYLGFGRDAMVYPDPAQGFELRLRQVLYSPFSTLILTTVGDTPPPAR 240  
 QY 241 EBEYLFVMDGFLAVWGFATIMSGSVYNNMTADAAPPDHALYKVKYKLVNRKLE 300  
 DB 241 EBEYLFVMDGFLAVWGFATIMSGSVYNNMTADAAPPDHALYKVKYKLVNRKLE 300  
 QY 301 RRYVDMYQHLQINKKMTNEVALIQHLPRLRAVAVSVHLSTSRVOITONCEASLLEEL 360  
 DB 301 RRYVDMYQHLQINKKMTNEVALIQHLPRLRAVAVSVHLSTSRVOITONCEASLLEEL 360  
 QY 361 VLKLPQYVSPGYYVCRKDDIGEMVYIIRGQLAVVADGITTQYAVLAGLGEISIIIN 420  
 DB 361 VLKLPQYVSPGYYVCRKDDIGEMVYIIRGQLAVVADGITTQYAVLAGLGEISIIIN 420  
 QY 421 IKGNSGNRRNTANIKSLGYSDFLCISKEDIREVLSYPOAQITMEKGRGRIILKNKLV 480  
 DB 421 IKGNSGNRRNTANIKSLGYSDFLCISKEDIREVLSYPOAQITMEKGRGRIILKNKLV 480  
 QY 481 NAEAAIATAOEATSLRGDQDLQDTKFAFLLELESSALKIYRIERLEWQTRMP 540  
 DB 481 NAEAAIATAOEATSLRGDQDLQDTKFAFLLELESSALKIYRIERLEWQTRMP 540  
 QY 541 MPEDLAADDEGEPEEGTSKDEGRASQSGPPGPE 575  
 DB 541 MPEDLAADDEGEPEEGTSKDEGRASQSGPPGPE 575

DB 541 MPEDLAADDEGEPEEGTSKDEGRASQSGPPGPE 575

RESULT 3  
 ABB07725  
 ID ABB07725 standard; protein; 575 AA.  
 XX  
 AC ABB07725;  
 XX  
 DT 10-JUN-2002 (first entry)  
 XX  
 DE Human cyclic nucleotide-gated cation channel subunit, CNG2B.  
 XX  
 KW Cyclic nucleotide-gated cation channel; CNG2B; CNG; cation channel;  
 KW cyclic nucleotide-gating; neuroprotective; cytoskeletal; antiviral;  
 KW gene therapy; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200214467-A2.  
 XX  
 PD 21-FEB-2002.  
 XX  
 PF 13-AUG-2001; 2001WO-US025392.  
 XX  
 PR 17-AUG-2000; 2000US-022623P.  
 XX  
 PR 10-AUG-2001; 2001US-00927267.  
 XX  
 PA (ICAG-) ICAGEN INC.  
 XX  
 PI Creech CD, Jegla TJ;  
 XX  
 DR MPI: 2002-269183/31.  
 XX  
 DR N-PSDB; ABA95279; ABA95280.  
 XX  
 XX New cyclic nucleotide gated cation channel nucleic acids, useful in gene  
 PT therapy for correcting acquired and inherited genetic defects, cancer and  
 PT viral infection.  
 XX  
 PS Claim 15; Fig 4; 78pp; English.  
 XX  
 CC The invention relates to a novel human cyclic nucleotide-gated cation  
 CC channel subunit, CNG2B. The polypeptide forms with at least one cyclic  
 CC nucleotide gated cation channel (CNG) alpha subunit, a cation channel  
 CC having the characteristic of cyclic nucleotide-gating. CNG2B polypeptides  
 CC are useful for testing inhibitors and activators of cyclic nucleotide-  
 CC gated cation channels, where such activators or inhibitors are useful as  
 CC pharmaceutical agents for treating diseases involving abnormal ion flux,  
 CC e.g. neurological disorders. CNG2B nucleic acids and polypeptides are  
 CC also useful for diagnostic applications for diseases involving abnormal  
 CC ion flux. CNG2B genes may be used in gene therapy to correct acquired and  
 CC inherited genetic defects, cancer and viral infection. CNG2B can be used  
 CC as an indicator of current flow in a particular direction, or as an  
 CC indirect reporter via attachment to a second reporter molecule, such as  
 CC green fluorescent protein. CNG2B modulators are useful for treating neu  
 CC logical diseases. The present sequence represents the human CNG2B  
 XX  
 XX Sequence 575 AA;  
 XX

Query Match 100.0%; Score 2989; DB 5; Length 575;  
 Best Local Similarity 100.0%; Pred. No. 8.7e-278;  
 Matches 575; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSODTKVKTSSPPAPSKARKLLPVLDPSSGDIYYWMLNTWFPVWYNIILIVCRACFPD 60  
 DB 1 MSODTKVKTSSPPAPSKARKLLPVLDPSSGDIYYWMLNTWFPVWYNIILIVCRACFPD 60  
 QY 61 LQHGVLVAMLVLDYSDLLYLDMVVRFRHTGFLBEGILVVDKGRISRRVYRTMSFFLDA 120  
 DB 61 LQHGVLVAMLVLDYSDLLYLDMVVRFRHTGFLBEGILVVDKGRISRRVYRTMSFFLDA 120  
 QY 121 SLMPDQVYVVRGPHPTPLRLRFLAPRLFEAFDSTETRTAYPNAFRIAKMLYIFVVI 180  
 DB 121 SLMPDQVYVVRGPHPTPLRLRFLAPRLFEAFDSTETRTAYPNAFRIAKMLYIFVVI 180

```
Dh 121 SLMPDVVYVRLGPHPTLRINRFLRAPRLFEAFDRTETRTAVNPAFRIAKMLYIFVVI 180
Qy 181 HNSCLYFALSRYLGFGRDAMVYPPDPAOPGPEERLRQYLSFYSSTLILTTVGDTTPPAR 240
Dh 181 HNSCLYFALSRYLGFGRDAMVYPPDPAOPGPEERLRQYLSFYSSTLILTTVGDTTPPAR 240
Qy 241 EEEYLFVWGDFLAVMGFATIMGSMSSVYNNMTADAFAFPDHALVKYMKLOHVNRKLE 300
Dh 241 EEEYLFVWGDFLAVMGFATIMGSMSSVYNNMTADAFAFPDHALVKYMKLOHVNRKLE 300
Qy 301 RRVLDWYOHLOINKKMTNEVAILLOHLPERRARAVAVSHLSTLSRVQIFONCEASLLEEL 360
Dh 301 RRVLDWYOHLOINKKMTNEVAILLOHLPERRARAVAVSHLSTLSRVQIFONCEASLLEEL 360
Qy 361 VLKLPQOTYSPGSEYVCKRGDIGEMYLIREGOLAVVADGITOYAVLAGLYFGELISIN 420
Dh 361 VLKLPQOTYSPGSEYVCKRGDIGEMYLIREGOLAVVADGITOYAVLAGLYFGELISIN 420
Qy 421 IKGNMGNRRNTANIKSLGYSDLCCLSKEDLREVLSYPOAQTIMKEGREILLKNNKLDV 480
Dh 421 IKGNMGNRRNTANIKSLGYSDLCCLSKEDLREVLSYPOAQTIMKEGREILLKNNKLDV 480
Qy 481 NAEAAEIALQEAATESRLRGDQDLDLQTKFARLLAELESSAKIAYIERLEWQTRMP 540
Dh 481 NAEAAEIALQEAATESRLRGDQDLDLQTKFARLLAELESSAKIAYIERLEWQTRMP 540
Qy 541 MPEDLAADDEGEPEEGTSKDEGRASQEGPPGPE 575
Dh 541 MPEDLAADDEGEPEEGTSKDEGRASQEGPPGPE 575

RESULT 4
ABU09091
ID ABU09091 standard; protein; 575 AA.
AC ABU09091;
DT 05-AUG-2003 (first entry)
DE Human transporter polypeptide.
KM Human; transporter.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Misc-difference 317 /note= "Encoded by TCC"
FT Misc-difference 432 /note= "Encoded by ACC"
FT Misc-difference 476 /note= "Encoded by AGC"
FT Misc-difference 553 /note= "Encoded by AAG"
FT /note= "Val substituted by Glu"
EN US2003013156-A1.
XX 16-JAN-2003.
PD 31-JUL-2002; 2002US-00207951.
PF 13-JUN-2000; 2000US-0211223P.
PR 14-DEC-2000; 2000US-00735932.
XX (APPL-) APPLERA CORP.
PI Guegler K, Ketchum KA, Di Francesco V, Beasley EM;
XX WPI; 2003-416799/39.
DR N-PSDB; ABX95978.
XX New transporter proteins related to cyclic nucleotide-gated ion channel
PT subfamily and polynucleotide encoding the protein for diagnosing,
```

PT treating diseases mediated by transporter protein and identifying modulators.

Claim 1, Fig 2A; 52pp; English.

CC The invention relates to an isolated human transporter polypeptide and  
CC the polynucleotide encoding it. The polypeptide is useful for identifying  
CC a modulator of the expression of the protein by contacting the protein  
CC with an agent and determining if the agent has modulated the function,  
CC activity or expression of the protein. The agent is administered to a  
CC host cell comprising an expression vector that expresses the protein. The  
CC polypeptide is also useful for identifying an agent that binds to the  
CC transporter protein. The polypeptide or condition mediated by a human  
CC models for the development of human therapeutic targets, to aid in the  
CC identification of therapeutic proteins and to serve as targets for the  
CC development of human therapeutic agents that modulate transporter  
CC activity in cells and tissues that express the transporter. The  
CC polypeptide is useful for raising antibodies or for eliciting another  
CC immune response, as a reagent in assays designed to quantitatively  
CC determine levels of the protein in biological fluids, as markers for  
CC tissues in which the corresponding protein is expressed and to identify  
CC the binding partner/ligand so as to develop a system to identify  
CC inhibitors of the binding interactions. This sequence represents the  
CC human transporter of the invention

Sequence 575 AA;

Query Match 100.0%; Score 2989; DB 6; Length 575;  
Best Local Similarity 100.0%; Pred. No. 8,7e-278;  
Matches 575; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy 1 MSODTKVKTTESSPPASRKRLPVLDSEGDYTYMMNTMVPVNNLILVCRACFPD 60
Dh 1 MSODTKVKTTESSPPASRKRLPVLDSEGDYTYMMNTMVPVNNLILVCRACFPD 60
Qy 61 LQHGVLVAMLVLDYTSDLVLYLDMVVRFRHTGFLQEGILVVDKGRISRYRTWSFLDIA 120
Dh 61 LQHGVLVAMLVLDYTSDLVLYLDMVVRFRHTGFLQEGILVVDKGRISRYRTWSFLDIA 120
Qy 121 SLMPDVVYVRLGPHPTLRINRFLRAPRLFEAFDRTETRTAVNPAFRIAKMLYIFVVI 180
Dh 121 SLMPDVVYVRLGPHPTLRINRFLRAPRLFEAFDRTETRTAVNPAFRIAKMLYIFVVI 180
Qy 181 HNSCLYFALSRYLGFGRDAMVYPPDPAOPGPEERLRQYLSFYSSTLILTTVGDTTPPAR 240
Dh 181 HNSCLYFALSRYLGFGRDAMVYPPDPAOPGPEERLRQYLSFYSSTLILTTVGDTTPPAR 240
Qy 241 EEEYLFVWGDFLAVMGFATIMGSMSSVYNNMTADAFAFPDHALVKYMKLOHVNRKLE 300
Dh 241 EEEYLFVWGDFLAVMGFATIMGSMSSVYNNMTADAFAFPDHALVKYMKLOHVNRKLE 300
Qy 301 RRVLDWYOHLOINKKMTNEVAILLOHLPERRARAVAVSHLSTLSRVQIFONCEASLLEEL 360
Dh 301 RRVLDWYOHLOINKKMTNEVAILLOHLPERRARAVAVSHLSTLSRVQIFONCEASLLEEL 360
Qy 361 VLKLPQOTYSPGSEYVCKRGDIGEMYLIREGOLAVVADGITOYAVLAGLYFGELISIN 420
Dh 361 VLKLPQOTYSPGSEYVCKRGDIGEMYLIREGOLAVVADGITOYAVLAGLYFGELISIN 420
Qy 421 IKGNMGNRRNTANIKSLGYSDLCCLSKEDLREVLSYPOAQTIMKEGREILLKNNKLDV 480
Dh 421 IKGNMGNRRNTANIKSLGYSDLCCLSKEDLREVLSYPOAQTIMKEGREILLKNNKLDV 480
Qy 481 NAEAAEIALQEAATESRLRGDQDLDLQTKFARLLAELESSAKIAYIERLEWQTRMP 540
Dh 481 NAEAAEIALQEAATESRLRGDQDLDLQTKFARLLAELESSAKIAYIERLEWQTRMP 540
Qy 541 MPEDLAADDEGEPEEGTSKDEGRASQEGPPGPE 575
Dh 541 MPEDLAADDEGEPEEGTSKDEGRASQEGPPGPE 575
```

RESULT	5
ABP55141	
ID	ABP55141 standard; protein, 575 AA.
XX	
AC	ABP55141;
DT	05-FEB-2003 (first entry)
XX	
DE	Human cyclic nucleotide-gated channel OCN2 subunit.
XX	
KW	OCN2; cyclic nucleotide-gated channel; human; cardiovascular disorder; neurological disorder; cardiant; vasotropic; antiarrhythmic; hypotensive; neuroprotective; nootropic; gene therapy.
OS	Homo sapiens.
XX	
FH	Key
FT	Domain
FT	/note= "transmembrane helix"
FT	64..86
FT	/note= "transmembrane helix"
FT	172..190
FT	/note= "transmembrane helix"
FT	218..236
FT	/note= "transmembrane helix"
FT	248..270
FT	/note= "transmembrane helix"
FT	375..392
FT	/note= "cyclic nucleotide-binding domain signature"
FT	413..437
FT	/note= "cyclic nucleotide-binding domain signature"
XX	
PN	WO200281689-A1.
XX	
PD	17-OCT-2002.
PF	19-FEB-2002; 2002MO-EP001726.
PR	20-FEB-2001; 2001US-0269402P. 13-NOV-2001; 2001US-033127P. 23-JAN-2002; 2002US-035003BP.
PR	(FARB ) BAYER AG.
PA	
PI	Zhu Z;
PS	WP1: 2003-046865/04. N-PSDB; ABV75870.
PT	New human cyclic nucleotide-gated channel OCN2 subunit polypeptide for treating, preventing or ameliorating a central nervous system disorder and cardiovascular disorder such as myocardial infarction.
PT	
PT	
PT	
XX	
PS	Claim 25; Fig 2; 112pp; English.
XX	
CC	The present sequence is the protein sequence of a novel human cyclic nucleotide-gated channel OCN2 subunit polypeptide, a human orthologue of rat olfactory cyclic nucleotide-gated channel OCN2 subunit, containing transmembrane and cyclic nucleotide-binding domains. The invention provides human OCN2 subunit polynucleotides and polypeptides, methods for their detection, expression vectors, host cells, and methods of screening for agents which decrease or regulate the activity of the OCN2 subunit. Claimed pharmaceutical compositions comprise an expression vector encoding the OCN2 subunit, or comprise a reagent which modulates the subunit's activity. These are used to treat a cardiovascular disorder or a central nervous system (CNS) disorder. Agents which modulate an activity of the OCN2 subunit include antibodies and antisense oligonucleotides (all claimed). The pharmaceutical compositions are useful for treating, preventing or ameliorating cardiovascular diseases such as congestive heart failure, myocardial infarction, ischemic diseases of the heart, atrial and ventricular arrhythmias, hypertensive vascular diseases, and peripheral vascular diseases and to screen for human cyclic nucleotide-gated channel OCN2 subunit activators and

Query Match	100.0%	Score 2989	DB 6	Length 575
Best Local Similarity	100.0%	Pred. No. 8.7e-278		
Matches 575	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Sequence 575 AA:				
Query	1	MSODTKVKTSTSSPPAPSKARKLPVLDP	SGDYVYVMTWTFPVYNYLIIVCRACFPD	60
Db	1	MSQDTKVKTSTSSPPAPSKARKLPVLDP	SGDYVYVMTWTFPVYNYLIIVCRACFPD	60
Qy	61	LOHGIVAMVLVDYSDLLYLIDMNVYRHTGFL	EGGILVVDKGRISRYRWTSPFLDA	120
Db	61	LOHGIVAMVLVDYSDLLYLIDMNVYRHTGFL	EGGILVVDKGRISRYRWTSPFLDA	120
Qy	121	SLMPDDVYVYVYLGPHTPPLRLNRLPRLA	RLEPAPRTERTYTPYAPRAXMLYFVYI	180
Db	121	SLMPDDVYVYVYLGPHTPPLRLNRLPRLA	RLEPAPRTERTYTPYAPRAXMLYFVYI	180
Qy	181	HMNSCLVYALRYLGFGRDAMVYPPAPG	GEFRLROYLYSEFSTLLITTVGDTPPAR	240
Db	181	HMNSCLVYALRYLGFGRDAMVYPPAPG	GEFRLROYLYSEFSTLLITTVGDTPPAR	240
Qy	241	EEEYLFVWGDPELLAVMGFATIMGSMSV	YINNTADAAFPYDHALVKKYMKLOHVNRKLE	300
Db	241	EEEYLFVWGDPELLAVMGFATIMGSMSV	YINNTADAAFPYDHALVKKYMKLOHVNRKLE	300
Qy	301	RRVIDWYOHLOINKKMTNEVALILOHL	PERLRAEVAVSHLSTLSHVQIFONCEASLLEEL	360
Db	301	RRVIDWYOHLOINKKMTNEVALILOHL	PERLRAEVAVSHLSTLSHVQIFONCEASLLEEL	360
Qy	361	VLKLIQPTYSPEGEYVCRKDIGOEYXI	IREGOLAVVADGITQYAVLGGALYFGEISLIN	420
Db	361	VLKLIQPTYSPEGEYVCRKDIGOEYXI	IREGOLAVVADGITQYAVLGGALYFGEISLIN	420
Qy	421	IKGNMNGRRNTANIKSLGYSDLFCLSK	EDLREVLSEYFPOAQTIMEKGREILLKNNKLDV	480
Db	421	IKGNMNGRRNTANIKSLGYSDLFCLSK	EDLREVLSEYFPOAQTIMEKGREILLKNNKLDV	480
Qy	481	NAAEAETILOEATSRRLGLDQQLDDLOT	KFRRLAELBESSALKIAYRERLEMTQREWP	540
Db	481	NAAEAETILOEATSRRLGLDQQLDDLOT	KFRRLAELBESSALKIAYRERLEMTQREWP	540
Qy	541	MPEDLAEBDDGEPEEGTSKDEGRASO	EGPPGPE	575
Db	541	MPEDLAEBDDGEPEEGTSKDEGRASO	EGPPGPE	575



Best Local Similarity 99.8%; Pred. No. 2.6e-277;  
Matches 574; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 MSODTRKVTETSSPPAPSKARLLPVLDPSSGDIYYWMLNTMVPVWYNYLIIIVCRACFPD 60
DB 1 MSODTRKVTETSSPPAPSKARLLPVLDPSSGDIYYWMLNTMVPVWYNYLIIIVCRACFPD 60
QY 61 LQHGVLVAVLVVDYSDLLYLDMVVRFTGFLGEGILVVDGKRISSRVYRTWSPFLDLA 120
DB 61 LQHGVLVAVLVVDYSDLLYLDMVVRFTGFLGEGILVVDGKRISSRVYRTWSPFLDLA 120
QY 121 SLMPDVVVYVRLGPHPTLRNLRLPAPRLFEAFDRTETRTAYPNAFRIAKMLYIFVYI 180
DB 121 SLMPDVVVYVRLGPHPTLRNLRLPAPRLFEAFDRTETRTAYPNAFRIAKMLYIFVYI 180
QY 181 HNNSCLYFALSRYLGGPDAMVYPPDPAQGFERLRQYLYSFYFSLITITVGDTPPPAR 240
DB 181 HNNSCLYFALSRYLGGPDAMVYPPDPAQGFERLRQYLYSFYFSLITITVGDTPPPAR 240
QY 241 EEEYLFMVGDFLAVMGFATIMGSMSSVLYNNMTADAAYPDHALVKYTKMLQHVNRKLE 300
DB 241 EEEYLFMVGDFLAVMGFATIMGSMSSVLYNNMTADAAYPDHALVKYTKMLQHVNRKLE 300
QY 301 REVIDMYOHLQINKKTEVAILOHLPERLRABAVAVSHLSTLSRVQIFONCEASLLEEL 360
DB 301 REVIDMYOHLQINKKTEVAILOHLPERLRABAVAVSHLSTLSRVQIFONCEASLLEEL 360
QY 361 VIKLOPQYTSPEGYCRKDKDIGOEMTIREGQLAVVADGQIYQYAVLGAIFYGEISIN 420
DB 361 VIKLOPQYTSPEGYCRKDKDIGOEMTIREGQLAVVADGQIYQYAVLGAIFYGEISIN 420
QY 421 IKGNSGNRRTANISLGYSDLFCLSKEDREVLSEYPOAQTMEKREIILKNMKLV 480
DB 421 IKGNSGNRRTANISLGYSDLFCLSKEDREVLSEYPOAQTMEKREIILKNMKLV 480
QY 481 NAEAAEIALQEAATESRLRGIDQDLQTKFARLLAELESSALKIAYRIERLEWQTRWP 540
DB 481 NAEAAEIALQEAATESRLRGIDQDLQTKFARLLAELESSALKIAYRIERLEWQTRWP 540
QY 541 MPEDLAEDDGEPEEGTSGKDEBGRASQSGPPGPE 575
DB 541 MPEDLAEDDGEPEEGTSGKDEBGRASQSGPPGPE 575

RESULT 8
AAM47673
ID AAM47673 standard; protein; 575 AA.
AC AAM47673;
XX
XX 21-FEB-2002 (first entry)
XX
XX DE MOL10b protein sequence.
XX
XX KM MOL; G-coupled protein-receptor; cardiomyopathy; atherosclerosis;
XX cell signal processing; metabolic disorder; diabetes; cancer; human;
XX neurodegenerative disorder; immune disorder; cardiac disorder;
XX lung disease; autoimmune disease; developmental disorder; antidiabetic;
XX Cystostatic; Neuroprotective; Antiatherosclerotic; Immunosuppressive;
XX Gene therapy; Vaccine; antiinflammatory; MOL10b.
XX
XX OS Homo sapiens.
XX
XX PN WO200181578-A2.
XX
XX PD 01-NOV-2001.
XX
XX PF 26-APR-2001; 2001WO-US013578.
XX
XX PR 26-APR-2000; 2000US-0200158P.
XX PR 28-APR-2000; 2000US-0200613P.
XX PR 01-MAY-2000; 2000US-0200780P.
XX PR 01-MAY-2000; 2000US-0201006P.

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PR 01-MAY-2000; 2000US-0201007P.
PR 01-MAY-2000; 2000US-0201236P.
PR 01-MAY-2000; 2000US-0201238P.
PR 02-MAY-2000; 2000US-0201186P.
PR 03-MAY-2000; 2000US-0201474P.
PR 03-MAY-2000; 2000US-0201508P.
PR 25-JUL-2000; 2000US-0220591P.
PR 15-SEP-2000; 2000US-0232678P.
PR 22-JAN-2001; 2001US-0263217P.
PR 30-JAN-2001; 2001US-0265160P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Vernet CAM, Fernandes ER, Gerlach V, Shinkens RA, Maljankar UM;
XX Bolog FL, Zehusen BD, Spytek KA, Majumder K, Tchernev VT;
XX Padigan M, Paturajan M, Burgess CE, Gangoli EA, Sathson G;
XX Rastelli L, Macdougall JR, Taupier RJ, Grose WM, Szekeres ES;
XX Alsbrook JP;
XX
XX WPI: 2002-049278/06.
XX N-PSDB; ABA04603.
XX
XX Novel G-protein coupled receptor-related polypeptides and polynucleotides
XX for diagnosing, preventing and treating cardiomyopathy, atherosclerosis,
XX disorders related to cell signal processing and for identifying
XX modulators.
XX
XX Claim 1; Page 79; 227pp; English.
XX
XX The present invention relates to novel G-coupled protein-receptor related
XX proteins and coding sequences (MOLX, where X is a number from 1 to 10,
XX ABA04589-ABA04603 and AAM47659-AAM47673). MOLX proteins and coding
XX sequences are useful for treating or preventing a MOLX-associated
XX disorder, such as cardiomyopathy, atherosclerosis, disorders related to
XX cell signal processing and metabolic pathway modulation, diabetes and
XX cancer. Additionally, MOLX proteins and coding sequences are useful for
XX preventing and treating a variety of disorders including metabolic
XX disorders, nutritional oedema, chronic and hereditary pancreaticitis,
XX obesity, infectious disease, anorexia, neurodegenerative disorders,
XX Alzheimer's disease, Parkinson's disease, stroke, immune disorders,
XX haematopoietic disorders and various dyslipidaemias, metabolic syndrome X
XX and wasting disorders associated with chronic diseases and cancers,
XX cardiac disorders, hypertension, hypercalcaemia, cirrhosis, angiodenesis,
XX and wound healing, trauma, glomerulonephritis, hyper and hypothyroidism,
XX multiple sclerosis, lung diseases including asthma, Crohn's disease,
XX scleroderma, autoimmune diseases, developmental disorders and neural tube
XX defects. The present sequence is the protein sequence for human MOL10b.
XX CC MOL10b protein is a cyclic nucleotide-gated olfactory channel-like
XX protein
XX
XX SO Sequence 575 AA;
XX
XX Query Match 99.8%; Score 2984; DB 5; Length 575;
XX Best Local Similarity 99.8%; Pred. No. 2.6e-277;
XX Matches 574; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

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DB      ||||| 241 EEEYLFMWGDFLLAWGFAITGSMSSVYNNMTADAAFYDPHALVKKMKMLQHVNRKLE 300
QY      ||||| 301 RRVIMVYQHLQINKKMTNEVALIQLPRLRAEVAVSVAHSLTISRVOIFONCEASLLEEL 360
DB      ||||| 301 RRVIMVYQHLQINKKMTNEVALIQLPRLRAEVAVSVAHSLTISRVOIFONCEASLLEEL 360
QY      ||||| 361 VKLQPPQYSPGEYVCRKGDIGQEMYYIRREGQLAVVADGGITQYAVLGAAGLYFGESLIIIN 420
DB      ||||| 361 VKLQPPQYSPGEYVCRKGDIGQEMYYIRREGQLAVVADGGITQYAVLGAAGLYFGESLIIIN 420
QY      ||||| 421 IKGNSGNRRNTANIKSLGYSDLPCLSKEDLREVLSEYPOAQTIMEKREILLKNNKLDV 480
DB      ||||| 421 IKGNSGNRRNTANIKSLGYSDLPCLSKEDLREVLSEYPOAQTIMEKREILLKNNKLDV 480
QY      ||||| 481 NAEAEIALQEAATESRLRGIDQQLDDLOTKFARLLAELESSALKIAYRIERLEWQTRWP 540
DB      ||||| 481 NAEAEIALQEAATESRLRGIDQQLDDLOTKFARLLAELESSALKIAYRIERLEWQTRWP 540
QY      ||||| 541 MPEDLAADDEGEPEEGTSKDEGRASQEGPPGPE 575
DB      ||||| 541 MPEDLAADDEGEPEEGTSKDEGRASQEGPPGPE 575

RESULT 9
ADJ87678 standard; protein; 575 AA.
ID      ADJ87678
AC      ADJ87678;
XX      06-MAY-2004 (first entry)
XX      G-coupled protein receptor-related protein #15.
DE      G-coupled protein receptor-related protein #15.
XX      novel protein; G-coupled protein receptor-related protein;
XX      cardiomyopathy; atherosclerosis; cell signal processing-related disorder;
XX      metabolic pathway modulation-related disorder; diabetes; cancer; stroke;
XX      Huntington's disease; epilepsy; anxiety; pain; hypercholesterolaemia;
XX      obesity; hypertension; Crohn's disease; systemic lupus erythematosus;
XX      viral infections; bacterial infection; parasitic infection;
XX      hyperthyroidism; hypothyroidism; Von Hippel-Lindau syndrome;
XX      Alzheimer's disease; tuberous sclerosis; hypercalcaemia; cerebral palsy.
XX      Unidentified.
XX      OS
XX      PN      MO2002102321-AA2.
XX      PD      27-DEC-2002.
XX      PF      18-JUN-2002; 2002MO-US019522.
XX      PR      18-JUN-2001; 2001US-0298994P.
XX      PR      18-OCT-2001; 2001US-0298134P.
XX      PR      06-JUN-2002; 2002US-00299134.
XX      PR      07-JUN-2002; 2002US-00298994.
XX      PA      (CURA-) CURAGEN CORP.
XX      PI      Anderson DW, Guo X, Gusev VY, Herrmann JL, Li L, Mezes PS,
XX      PI      Pena CE, Spaderna SK, Zhong M;
XX      DR      WPI; 2003-167441/16.
XX      DR      N-PSDB; ADJ87677.
XX      PT      New MOX polypeptides and polymucleotides, useful in gene therapy,
XX      PT      particularly for treating or preventing e.g. cardiomyopathy,
XX      PT      atherosclerosis, diabetes, adenoma, brain tumor, breast cancer, prostate
XX      PT      cancer, stroke or pain.
XX      PS      Claim 1; SEQ ID NO 30; 378bp; English.
XX      CC      The invention comprises the amino acid and coding sequences of novel G-

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CC      coupled protein receptor-related (MOL) proteins. The DNA and protein
CC      sequences of the invention are useful for treating or preventing a MOL-
CC      associated disorder, such as: cardiomyopathy, atherosclerosis, disorders
CC      associated with cell signal processing and metabolic pathway modulation,
CC      or diabetes. The DNA and protein sequences are also useful for the
CC      treatment of: cancer, stroke, Huntington's disease, epilepsy, anxiety,
CC      pain, hypercholesterolaemia, obesity, hypertension, Crohn's disease,
CC      systemic lupus erythematosus, viral infections, bacterial infections,
CC      parasitic infections, hyperthyroidism, hypothyroidism, Von Hippel-Lindau
CC      syndrome, Alzheimer's disease, tuberous sclerosis, hypercalcaemia, or
CC      cerebral palsy. The present amino acid sequence represents a MOL protein
CC      of the invention.
SQ      Sequence 575 AA;
QY      Query Match      99.8%; Score 2984; DB 7; Length 575;
QY      Best Local Similarity 99.8%; Pred. No. 2.6e-27;
QY      Matches 574; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DB      1 MSQDTKYKTTSSPPAPSKARKLLPVLDPSGDIYYMMNTMPPVMTNLIIVCRACFPD 60
QY      1 LQHGIVAMLVLDYTSLLYLDMVVRFTGFLQGIIVVDKGRISRYRTWSFFDLA 120
DB      61 LQHGIVAMLVLDYTSLLYLDMVVRFTGFLQGIIVVDKGRISRYRTWSFFDLA 120
QY      121 SLMPDVVYVRLGPHPTFLRLNRLRAPRLFEAFDRTEFTRAVFNARIKMLMIFVVI 180
DB      121 SLMPDVVYVRLGPHPTFLRLNRLRAPRLFEAFDRTEFTRAVFNARIKMLMIFVVI 180
QY      181 HMNSCLYPALSRVYGFGRDAWVYDPPAOPGPERLRROYLYSFYSTLILTTVGDTPPPAR 240
DB      181 HMNSCLYPALSRVYGFGRDAWVYDPPAOPGPERLRROYLYSFYSTLILTTVGDTPPPAR 240
QY      241 EEEYLFMWGDFLLAWGFAITGSMSSVYNNMTADAAFYDPHALVKKMKMLQHVNRKLE 300
DB      241 EEEYLFMWGDFLLAWGFAITGSMSSVYNNMTADAAFYDPHALVKKMKMLQHVNRKLE 300
QY      301 RRVIMVYQHLQINKKMTNEVALIQLPRLRAEVAVSVAHSLTISRVOIFONCEASLLEEL 360
DB      301 RRVIMVYQHLQINKKMTNEVALIQLPRLRAEVAVSVAHSLTISRVOIFONCEASLLEEL 360
QY      361 VKLQPPQYSPGEYVCRKGDIGQEMYYIRREGQLAVVADGGITQYAVLGAAGLYFGESLIIIN 420
DB      361 VKLQPPQYSPGEYVCRKGDIGQEMYYIRREGQLAVVADGGITQYAVLGAAGLYFGESLIIIN 420
QY      421 IKGNSGNRRNTANIKSLGYSDLPCLSKEDLREVLSEYPOAQTIMEKREILLKNNKLDV 480
DB      421 IKGNSGNRRNTANIKSLGYSDLPCLSKEDLREVLSEYPOAQTIMEKREILLKNNKLDV 480
QY      481 NAEAEIALQEAATESRLRGIDQQLDDLOTKFARLLAELESSALKIAYRIERLEWQTRWP 540
DB      481 NAEAEIALQEAATESRLRGIDQQLDDLOTKFARLLAELESSALKIAYRIERLEWQTRWP 540
QY      541 MPEDLAADDEGEPEEGTSKDEGRASQEGPPGPE 575
DB      541 MPEDLAADDEGEPEEGTSKDEGRASQEGPPGPE 575

RESULT 10
ABU09778 standard; protein; 575 AA.
ID      ABU09778
AC      ABU09778;
XX      05-AUG-2003 (first entry)
XX      Human transporter variant polypeptide.
XX      Human; transporter.
XX      OS      Homo sapiens.

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XX Key Location/Qualifiers
FH Misc-difference 317 /note= "Encoded by TCC"
FT Misc-difference 432 /note= "Encoded by ACC"
FT Misc-difference 476 /note= "Encoded by AGC"
FT Misc-difference 553 /note= "Glu substituted by Val"
FT US2003013156-A1.
XX
XX 16-JAN-2003.
XX
XX 31-JUL-2002; 2002US-00207951.
XX
XX 13-JUN-2000; 2000US-0211223P.
XX 14-DEC-2000; 2000US-00735932.
XX (APPL-) APPLERA CORP.
XX Guejler K, Ketchum KA, Di Francesco V, Beasley EM;
XX WPI; 2003-416799/39.
XX
XX New transporter proteins related to cyclic nucleotide-gated ion channel
XX subfamily and polynucleotide encoding the protein for diagnosing,
XX treating diseases mediated by transporter protein and identifying
XX modulators.
XX
XX Disclosure; Page: 52pp; English.
XX
XX The invention relates to an isolated human transporter polypeptide and
XX the polynucleotide encoding it. The polypeptide is useful for identifying
XX a modulator of the expression of the protein by contacting the protein
XX with an agent and determining if the agent has modulated the function,
XX activity or expression of the protein. The agent is administered to a
XX host cell comprising an expression vector that expresses the protein. The
XX polypeptide is also useful for identifying an agent that binds to the
XX transporter protein. The polypeptide and polynucleotide are useful as
XX models for the development of human therapeutic targets, to aid in the
XX identification of therapeutic proteins and to serve as targets for the
XX development of human therapeutic agents that modulate transporter
XX activity in cells and tissues that express the transporter. The
XX polypeptide is useful for raising antibodies or for eliciting another
XX immune response, as a reagent in assays designed to quantitatively
XX determine levels of the protein in biological fluids, as markers for
XX tissues in which the corresponding protein is expressed and to identify
XX the binding partner/ligand so as to develop a system to identify
XX inhibitors of the binding interactions. This sequence represents a human
XX transporter variant polypeptide of the invention. Note: This sequence is
XX not featured in the specification but was derived from the polypeptide
XX shown in ABU09091
XX
XX Sequence 575 AA;
SQ
Query Match 99.8%; Score 2982; DB 6; Length 575;
Best Local Similarity 99.8%; Pred. No. 4.1e-277;
Matches 574; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MSQDTRKVTSSPPAPSKARKLLPVLDSGYYWMLTMMVFPVWYNLIIVCRACFPD 60
DB 1 MSQDTRKVTSSPPAPSKARKLLPVLDSGYYWMLTMMVFPVWYNLIIVCRACFPD 60
QY 61 LQHGVLAVMLVDYSDLLYLDMVVRFTGTGLEQILVVDKGRISRRVYRTWSFPLDA 120
DB 61 LQHGVLAVMLVDYSDLLYLDMVVRFTGTGLEQILVVDKGRISRRVYRTWSFPLDA 120
QY 121 SIMPTDVVYVRLGPHPTTLRLNRFAPRLFEAFDRTETRTAVPNAFRIAKMLYFVVI 180
DB 121 SIMPTDVVYVRLGPHPTTLRLNRFAPRLFEAFDRTETRTAVPNAFRIAKMLYFVVI 180

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QY 181 HNSCLYFALSRVIGFGDAMVYPPAPQGFERLROLYSFYSTLLITLTVGDTPPPAR 240
DB 181 HNSCLYFALSRVIGFGDAMVYPPAPQGFERLROLYSFYSTLLITLTVGDTPPPAR 240
QY 241 EEEYLFVWGDFLLAVMGFATIMGSSSVIYNNNTDAAFPYDHALVKKYMKIQHVNKLE 300
DB 241 EEEYLFVWGDFLLAVMGFATIMGSSSVIYNNNTDAAFPYDHALVKKYMKIQHVNKLE 300
QY 301 RRVIDWYHQLQINKKMTNEVALIQHLPERLAEVAVSVHLSTLSVQIFQNCESLLEL 360
DB 301 RRVIDWYHQLQINKKMTNEVALIQHLPERLAEVAVSVHLSTLSVQIFQNCESLLEL 360
QY 361 VLKLPQYTSPEGYVCRKADIGQEMYYIIREGLAVVADGITQYAVLAGYFGEISLIN 420
DB 361 VLKLPQYTSPEGYVCRKADIGQEMYYIIREGLAVVADGITQYAVLAGYFGEISLIN 420
QY 421 IKGNMSGNRRRTANIKSLGYSDLFCLSKEDLREVLSEYPOAQTIMKEKREIILKNKLDV 480
DB 421 IKGNMSGNRRRTANIKSLGYSDLFCLSKEDLREVLSEYPOAQTIMKEKREIILKNKLDV 480
QY 481 NAEAEIQLQENTESRLGLDQQLDLDLQTKPARLLAELESSLKIAYRIERLEMTREMP 540
DB 481 NAEAEIQLQENTESRLGLDQQLDLDLQTKPARLLAELESSLKIAYRIERLEMTREMP 540
QY 541 MPEDLAEDDEGEPEEGTSKDEGRASQEGPPGPE 575
DB 541 MPEDLAEDDEGEPEEGTSKDEGRASQEGPPGPE 575

RESULT 11
AAM47672
ID AAM47672 standard; protein; 578 AA.
XX
XX AAM47672;
XX
XX 21-FEB-2002 (first entry)
XX
XX MOL10a protein sequence.
XX
XX MOL1; G-coupled protein-receptor; cardiomyopathy; atherosclerosis;
XX cell signal processing; metabolic disorder; diabetes; cancer;
XX neurodegenerative disorder; immune disorder; cardiac disorder;
XX lung disease; autoimmune disease; developmental disorder; anti-diabetic;
XX Cystostatic; Neuroprotective; Antiatherosclerotic; Immunosuppressive;
XX Gene therapy; Vaccine; antiinflammatory; MOL10a.
XX
XX Unidentified.
XX
XX MO200181578-A2.
XX
XX 01-NOV-2001.
XX
XX 26-APR-2001; 2001WO-US013578.
XX
XX 26-APR-2000; 2000US-0200158P.
XX 28-APR-2000; 2000US-0200613P.
XX 28-APR-2000; 2000US-0200780P.
XX 01-MAY-2000; 2000US-0201006P.
XX 01-MAY-2000; 2000US-0201007P.
XX 01-MAY-2000; 2000US-0201236P.
XX 01-MAY-2000; 2000US-0201238P.
XX 02-MAY-2000; 2000US-0201186P.
XX 03-MAY-2000; 2000US-0201474P.
XX 03-MAY-2000; 2000US-0201508P.
XX 25-JUL-2000; 2000US-0220591P.
XX 15-SEP-2000; 2000US-0232678P.
XX 22-JAN-2001; 2001US-0263217P.
XX 30-JAN-2001; 2001US-0265160P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Vernet CAM, Fernandes ER, Gerlach V, Shinkets RA, Maljankar UM;
PI

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PI Bol'dog FL, Zernusen BD, Spytek KA, Majumder K, Tchernev VT;  
 PI Padigaru M, Paturajan M, Burgess CE, Gangolli EA, Smithson G;  
 PI Rastelli L, Macdougall JR, Taupier RJ, Grose WM, Szekeres ES;  
 PI Alsobrook JP;  
 XX  
 DR WPI; 2002-049228/06.  
 DR N-PSDB; ABA04602.

PT Novel G-protein coupled receptor-related polypeptides and polynucleotides  
 PT for diagnosing, preventing and treating cardiomyopathy, atherosclerosis,  
 PT disorders related to cell signal processing and for identifying  
 PT modulators.

XX  
 PS Claim 1; Page 77; 227pp; English.

CC The present invention relates to novel G-coupled protein-receptor related  
 CC proteins and coding sequences (MOLX, where X is a number from 1 to 10,  
 CC ABA04589-ABA04603 and AAM47659-AAM47673). MOLX proteins and coding  
 CC sequences are useful for treating or preventing a MOLX-associated  
 CC disorder, such as cardiomyopathy, atherosclerosis, disorders related to  
 CC cell signal processing and metabolic pathway modulation, diabetes and  
 CC cancer. Additionally, MOLX proteins and coding sequences are useful for  
 CC preventing and treating a variety of disorders including metabolic  
 CC disorders, nutritional oedema, chronic and hereditary pancreatitis,  
 CC obesity, infectious disease, anorexia, neurodegenerative disorders,  
 CC Alzheimer's disease, Parkinson's disease, stroke, immune disorders,  
 CC haematopoietic disorders and various dyslipidaemias, metabolic syndrome X  
 CC and wasting disorders associated with chronic diseases and cancers,  
 CC cardiac disorders, hypertension, hypercalcaemia, cirrhosis, angiodysplasia  
 CC and wound healing, trauma, glomerulonephritis, hyper and hypothyroidism,  
 CC multiple sclerosis, lung diseases including asthma, Crohn's disease,  
 CC scleroderma, autoimmune diseases, developmental disorders and neural tube  
 CC defects. The present sequence is the protein sequence for MOL10a. MOL10a  
 CC protein is a cyclic nucleotide-gated olfactory channel-like protein  
 XX  
 XX Sequence 578 AA;

Query Match 98.9%; Score 2957.5; DB 5; Length 578;  
 Best Local Similarity 99.5%; Pred. No. 9.4e-275;  
 Matches 575; Conservative 0; Mismatches 0; Indels 3; Gaps 3;

QY 1 MSQDTRKVTETSSPPAPSKA-RKLPLVLDPSGDYYYMMNTMVFVWNLIIIVCRACP 59  
 DB 1 MSQDTRKVTETSSPPAPSKARKLLPVLDPSCDYIWMNTMVFVWNLIIIVCRACP 60  
 QY 60 DLQHGIVLAVMLVLDYTSLLIYLDNVAERHT-GELEGILVVDKGRISRRYRWSPFLD 118  
 DB 61 DLQHGIVLAVMLVLDYTSLLIYLDNVAERHTGEGLEGILVVDKGRISRRYRWSPFLD 120  
 QY 119 LASLMPDVTVVYRLQPHPTLRLNRFAPRLFAFPDTERTRAYPNAFRAXKMLYIFV 178  
 DB 121 LASLMPDVTVVYRLQPHPTLRLNRFAPRLFAFPDTERTRAYPNAFRAXKMLYIFV 180  
 QY 179 VIHNSCIYFALSYRLGFGDAMVYPDPAQGFERLRQVLYSFFSTLLITVGDTPPP 238  
 DB 181 VIHNSCIYFALSYRLGFGDAMVYPDPAQGFERLRQVLYSFFSTLLITVGDTPPP 240  
 QY 239 AREEYLFVWGDFLAVWGFAFMGSMSSVYVNTADAAVPPHAIYKMKLQHVNRK 298  
 DB 241 AREEYLFVWGDFLAVWGFAFMGSMSSVYVNTADAAVPPHAIYKMKLQHVNRK 300  
 QY 299 LERRIVIMYQHLQINKKMTNEVALIQLPRLRAVAVSVHLSTLSVQIFONCEASLLE 358  
 DB 301 LERRIVIMYQHLQINKKMTNEVALIQLPRLRAVAVSVHLSTLSVQIFONCEASLLE 360  
 QY 359 ELVYLKLPQYTSREBYVCRKDKIQEYIIRREGOLAVVADGITYAVLAGLYFGESL 418  
 DB 361 ELVYLKLPQYTSREBYVCRKDKIQEYIIRREGOLAVVADGITYAVLAGLYFGESL 420  
 QY 419 INIK-GNMSGNRRRANIKSLGYSDLPCLSKEDLREVLSEVPOQOTMEEGRETIILKMK 477  
 DB 421 INIK-GNMSGNRRRANIKSLGYSDLPCLSKEDLREVLSEVPOQOTMEEGRETIILKMK 480

QY 478 LVNABAEIALQETESRLRGLDQDLDTQKFARLAEISSALKIAYRIERLEMQTR 537  
 DB 481 LVNABAEIALQETESRLRGLDQDLDTQKFARLAEISSALKIAYRIERLEMQTR 540  
 QY 538 EWPMPEDLAEADDEPEEGTSGKEEGRASQSGPPGPE 575  
 DB 541 EWPMPEDLAEADDEPEEGTSGKEEGRASQSGPPGPE 578

RESULT 12  
 ADJ87676  
 ID ADJ87676 standard; protein; 578 AA.  
 XX  
 AC ADJ87676;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE G-coupled protein receptor-related protein #14.

XX novel protein; G-coupled protein receptor-related protein;  
 KW cardiomyopathy; atherosclerosis; cell signal processing-related disorder;  
 KW metabolic pathway modulation-related disorder; diabetes; cancer; stroke;  
 KW Huntington's disease; epilepsy; anxiety; pain; hypercholesterolaemia;  
 KW obesity; hypertension; Crohn's disease; systemic lupus erythematosus;  
 KW viral infections; bacterial infection; parasitic infection;  
 KW hyperthyroidism; hypothyroidism; Von Hippel-Lindau syndrome;  
 KW Alzheimer's disease; tuberculous sclerosis; hypercalcaemia; cerebral palsy.  
 OS Unidentified.  
 XX  
 XX MO2002102321-A2.  
 XX  
 XX 18-JUN-2002; 2002MO-US019522.  
 XX  
 XX 18-JUN-2001; 2001US-0298994P.  
 XX 18-JUN-2001; 2001US-0299134P.  
 XX 04-OCT-2001; 2001US-00972446.  
 XX 06-JUN-2002; 2002US-00299134.  
 XX 07-JUN-2002; 2002US-00298994.  
 XX  
 XX (CURA-) CURAGEN CORP.  
 XX  
 XX Anderson DW, Guo X, Gusev VY, Herrmann JL, Li L, Mezes PS;  
 PI Pena CEA, Spaderna SK, Zhong M;  
 XX N-PSDB; ADJ87675.  
 DR WPI; 2003-167441/16.  
 XX

PT New MOLX polypeptides and polynucleotides, useful in gene therapy,  
 PT particularly for treating or preventing e.g. cardiomyopathy,  
 PT atherosclerosis, diabetes, adenoma, brain tumor, breast cancer, prostate  
 PT cancer, stroke or pain.  
 XX  
 PS Claim 1; SEQ ID NO 28; 378pp; English.

XX The invention comprises the amino acid and coding sequences of novel G-  
 CC coupled protein receptor-related (MOL) proteins. The DNA and protein  
 CC sequences of the invention are useful for treating or preventing a MOL-  
 CC associated disorder, such as: cardiomyopathy, atherosclerosis, disorders  
 CC associated with cell signal processing and metabolic pathway modulation,  
 CC or diabetes. The DNA and protein sequences are also useful for the  
 CC treatment of: cancer, stroke, Huntington's disease, epilepsy, anxiety,  
 CC pain, hypercholesterolaemia, obesity, hypertension, Crohn's disease,  
 CC systemic lupus erythematosus, viral infections, bacterial infections,  
 CC parasitic infections, hyperthyroidism, hypothyroidism, Von Hippel-Lindau  
 CC syndrome, Alzheimer's disease, tuberculous sclerosis, hypercalcaemia, or  
 CC cerebral palsy. The present amino acid sequence represents a MOL protein  
 CC of the invention.

XX Sequence 578 AA;



Query Match 98.9%; Score 2957.5; DB 7; Length 578;  
 Best Local Similarity 99.5%; Pred. No. 9.4e-275;  
 Matches 575; Conservative 0; Mismatches 0; Indels 3; Gaps 3;

QY 1 MSQDTKVTETSSPPAPSKA-RKLLPVLDPGSDYYWMNTMVPVMTNLLVCRACP 59  
 DB 1 MSQDTKVTETSSPPAPSKARKLLPVLDPGSDYYWMNTMVPVMTNLLVCRACP 60  
 QY 60 DLQHGVLAVMLVDLDTSLLLYLDLVVVRPHT-GELEGGLVVDKGRISGRYRTSSFLD 118  
 DB 61 DLQHGVLAVMLVDLDTSLLLYLDLVVVRPHTGFLGGLVVDKGRISGRYRTSSFLD 120  
 QY 119 LASLMPDVVYVRLGPHPTLRLNRLFLAPRLFEAFDRTETRTAYPNAPRIAKMLYIFV 178  
 DB 121 LASLMPDVVYVRLGPHPTLRLNRLFLAPRLFEAFDRTETRTAYPNAPRIAKMLYIFV 180  
 QY 179 VIHNNSCLYFALSRYLFGGRDAVYVPPAPQPGFERLRQYLYSPYFSTLLITVGDTPPP 238  
 DB 181 VIHNNSCLYFALSRYLFGGRDAVYVPPAPQPGFERLRQYLYSPYFSTLLITVGDTPPP 240  
 QY 229 AREEYFLMWGDFLLAVNGFATIMGSMSSVYINMTADAAFPDHALYKKYMKLOHVRK 298  
 DB 241 AREEYFLMWGDFLLAVNGFATIMGSMSSVYINMTADAAFPDHALYKKYMKLOHVRK 300  
 QY 299 LERRVYDWOHLQINKKMTNEVALIQHLPERLRAEVAVSHLSTSRVQIFONCEASLLE 358  
 DB 301 LERRVYDWOHLQINKKMTNEVALIQHLPERLRAEVAVSHLSTSRVQIFONCEASLLE 360  
 QY 359 ELVLKLPQYVSPGEYVCRKQDQIGQEMYTIREGQLAVVADGDTYAVLAGLYFGEISI 418  
 DB 361 ELVLKLPQYVSPGEYVCRKQDQIGQEMYTIREGQLAVVADGDTYAVLAGLYFGEISI 420  
 QY 419 INIK-GNMSGNRRNTANISLGSDFCLSKEDLREVLSEYPAQITMEKKEEILLKMK 477  
 DB 421 INIKGNMSGNRRNTANISLGSDFCLSKEDLREVLSEYPAQITMEKKEEILLKMK 480  
 QY 478 LDVNAEAEIALQAEATESRLRGDLDOQLDLOTKFARLLAELESSALKIAYRIERLEMQR 537  
 DB 481 LDVNAEAEIALQAEATESRLRGDLDOQLDLOTKFARLLAELESSALKIAYRIERLEMQR 540  
 QY 538 EWPMPEDLAEDDEGEPEEGTSKDEEGRASQEGPPE 575  
 DB 541 EWPMPEDLAEDDEGEPEEGTSKDEEGRASQEGPPE 578

RESULT 13  
 ADN38409  
 ID ADN38409 standard; protein; 578 AA.  
 AC ADN38409;  
 XX  
 DT 17-JUN-2004 (first entry)  
 DE  
 XX  
 DE Novel human polynucleotide MO10a.  
 XX  
 KM anti-HIV; cytostatic; antiarteriosclerotic; antidiabetic; antiaethmatic;  
 KM antiinflammatory; haemostatic; hypotensive; neuroprotective; anorectic;  
 KM nootropic; antidepressant; immunosuppressive; antibacterial; vitruce;  
 KM fungicide; protozoacide; tranquilizer; anticonvulsant; osteopathic;  
 KM analgesic; antiparkinsonian; dermatological; antifertility;  
 KM cerebroprotective; antidiabetic; MOX-associated disorder;  
 KM cardiomyopathy; atherosclerosis; diabetes; cell signal processing;  
 KM metabolic pathway modulation; cancer; Von Hippel-Lindau syndrome;  
 KM Alzheimer's disease; stroke; tuberos sclerosis; hypercalcaemia;  
 KM Parkinson's disease; Huntington's disease; cerebral palsy; epilepsy;  
 KM Leshch-Vyhan syndrome; multiple sclerosis; ataxia-telangiectasia;  
 KM leukodystrophy; addiction; anxiety; depression; pain; obesity;  
 KM Crohn's disease; osteoporosis; inflammatory bowel disease; infertility;  
 KM hypertension; scleroderma; haemophilia; pancreatitis; autoimmune disease;  
 KM asthma; arthritis; immunodeficiency; HIV; infection;  
 KM graft-versus-host disease; gene therapy; vaccine; tissue typing;  
 KM pharmacogenomic; human.  
 XX

OS Homo sapiens.  
 XX  
 XX US2004029220-A1.  
 XX  
 PD 12-FEB-2004.  
 XX  
 PF 18-JUN-2002; 2002US-00174333.  
 XX  
 PR 26-APR-2000; 2000US-0200158P.  
 PR 28-APR-2000; 2000US-0200613P.  
 PR 28-APR-2000; 2000US-0200780P.  
 PR 01-MAY-2000; 2000US-0201006P.  
 PR 01-MAY-2000; 2000US-0201007P.  
 PR 01-MAY-2000; 2000US-0201236P.  
 PR 01-MAY-2000; 2000US-0201238P.  
 PR 02-MAY-2000; 2000US-0201186P.  
 PR 03-MAY-2000; 2000US-0201474P.  
 PR 03-MAY-2000; 2000US-0201508P.  
 PR 25-JUL-2000; 2000US-0220591P.  
 PR 15-SEP-2000; 2000US-0232678P.  
 PR 22-JAN-2001; 2001US-0263217P.  
 PR 30-JAN-2001; 2001US-0265160P.  
 PR 16-FEB-2001; 2001US-0265311P.  
 PR 25-APR-2001; 2001US-00842758.  
 PR 18-JUN-2001; 2001US-0298994P.  
 PR 07-JUN-2002; 2002US-0366837P.  
 XX  
 PA (VERN/) VERNET C A M.  
 PA (FERN/) FERNANDES E R.  
 PA (GERL/) GERLACH V.  
 PA (SHIM/) SHIMKETS R A.  
 PA (MALY/) MALYANKAR U M.  
 PA (BOLD/) BOLDOS F L.  
 PA (ZERH/) ZERHUSEN B D.  
 PA (SPYT/) SPYTEK K A.  
 PA (MAJU/) MAJUMDER K T.  
 PA (TCHE/) TCHERNEV V T.  
 PA (PADI/) PADIGARU M.  
 PA (PAT/) PATIRAJAN M.  
 PA (BURG/) BURGESS C E.  
 PA (GANG/) GANGOLLI E A.  
 PA (SMIT/) SMITHSON G.  
 PA (RAST/) RASTELLI L.  
 PA (MACD/) MACDOUGALL J R.  
 PA (TAUP/) TAUPIER R J.  
 PA (GROS/) GROSSE W M.  
 PA (SZEK/) SZEKERES E S.  
 PA (ALSO/) ALSOBROOK J P.  
 PA (ANDE/) ANDERSON D W.  
 PA (GUOX/) GUO X.  
 PA (LILL/) LI L.  
 PA (ZHON/) ZHONG M.  
 XX  
 PI Vernet CAM, Fernandes ER, Gerlach V, Shinkets RA, MalYankar UM;  
 PI Boldog FL, Zehhusen BD, Spytek KA, Majumder K, Tchernev VT;  
 PI Padigar M, Patirajan M, Burgess CE, Gangolli EA, Smithson G;  
 PI Rastelli L, MacDougall JR, Taupier RJ, Grose WM, Szekeres ES;  
 PI Alsobrook JP, Anderson DW, Guo X, Li L, Zhong M;  
 DR WPI; 2004-179668/17.  
 DR N-PSDB; ADN38408.  
 PT New isolated molecule (MOIX) polypeptide, useful for diagnosing, treating  
 PT or preventing MOIX-associated diseases, such as infarction,  
 PT atherosclerosis, diabetes, multiple sclerosis, Crohn's disease or cancer.  
 XX  
 XX Claim 1, SEQ ID NO 28; 212pp; English.  
 CC The invention describes an isolated molecule (MOIX) polypeptide. The MOIX  
 CC polypeptide, MOIX nucleic acid and antibody are useful for treating,  
 CC preventing or alleviating a MOIX-associated disorder or a pathological  
 CC state in a subject, particularly a human. In particular, the disorder is  
 CC cardiomyopathy, atherosclerosis, diabetes, or a disorder related to cell

CC signal processing and metabolic pathway modulation. The MOIX polypeptide  
 CC and nucleic acid are also useful for diagnosing the presence of MOIX,  
 CC predisposition to a disease associated with altered levels of MOIX,  
 CC particularly cancer. The MOIX nucleic acid and polypeptide are especially  
 CC useful in the manufacture of a medicament for therapeutic or prophylactic  
 CC applications for disorders associated with aberrant MOIX expression or  
 CC activity, e.g. Von Hippel-Lindau syndrome, Parkinson's disease, stroke,  
 CC tuberous sclerosis, hypercalcaemia, Huntington's  
 CC disease, cerebral palsy, epilepsy, Lesch-Nyhan syndrome, multiple  
 CC sclerosis, ataxia-telangiectasia, leukodystrophies, addiction, anxiety,  
 CC depression, pain, obesity, Crohn's disease, osteoporosis, inflammation,  
 CC bowel disease, infertility, hypertension, scleroderma, hemophilia,  
 CC pancreaticitis, autoimmune disease, asthma, arthritis, immunodeficiencies,  
 CC HIV, viral, fungal, bacterial or protozoal infections, or graft-versus-  
 CC host disease. The DNA encoding the protein is useful in gene therapy for  
 CC treating the above conditions. This is the amino acid sequence of a novel  
 CC human MOIX polypeptide.

XX Sequence 578 AA:

Query Match 98.9%; Score 2957.5; DB 8; Length 578;  
 Best Local Similarity 99.5%; Pred. No. 9.4e-275;  
 Matches 575; Conservative 0; Mismatches 0; Indels 3; Gaps 3;

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QY 1 MSODTKVKTTESSPPAPSKA-RKLPLVLDPSGDYYTWMNTNVFPVMNLLIVGRACP 59
DB 1 MSODTKVKTTESSPPAPSKARRKLPLVLDPSGDYYTWMNTNVFPVMNLLIVGRACP 60
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DB 61 DLQHGVLAVMLVDYTSDLLVLDWVFRHTGFLGGLVVDKGRISRRYRTSFLD 120
QY 119 LASLPPTDYYVRLGPHPTTLNLFRLAPLFEAPDRTETRTAVPNAFRIAKMLYIFV 178
DB 121 LASLPPTDYYVRLGPHPTTLNLFRLAPLFEAFDTEETRTAVPNAFRIAKMLYIFV 180
QY 179 VTHMNSCLYFALSRYLGFGRDAMVPPDPAQPGFEELRROYLYSPFESTLLITVGDTPPP 238
DB 181 VTHMNSCLYFALSRYLGFGRDAMVPPDPAQPGFEELRROYLYSPFESTLLITVGDTPPP 240
QY 239 AREEYLLFWGDFLLAVMGFATMGSSSVIYNNMTADAAFPDHALVKKYMKLQHVNRK 298
DB 241 AREEYLLFWGDFLLAVMGFATMGSSSVIYNNMTADAAFPDHALVKKYMKLQHVNRK 300
QY 299 LERRVIDMYQHLLQNKKTNEVALIQLPERLRAEVANSVHLSTLSRVQIFONCEASILE 358
DB 301 LERRVIDMYQHLLQNKKTNEVALIQLPERLRAEVANSVHLSTLSRVQIFONCEASILE 360
QY 359 ELVTLQOPQYSPGEYVCRKGDIGQEMYIIREGOLAVVADGITOYAVLAGLFGESIT 418
DB 361 ELVTLQOPQYSPGEYVCRKGDIGQEMYIIREGOLAVVADGITOYAVLAGLFGESIT 420
QY 419 INIK-GNNSGNRRNTAKSLGSDLPCLSKEDLREVLSEYPOAQTIWEKREITLMMNK 477
DB 421 INIKGNNSGNRRNTAKSLGSDLPCLSKEDLREVLSEYPOAQTIWEKREITLMMNK 480
QY 478 LDVNAEAELALQATATESRLGLDQDDLOTQFARLLAEESALKIARIENLEWQTR 537
DB 481 LDVNAEAELALQATATESRLGLDQDDLOTQFARLLAEESALKIARIENLEWQTR 540
QY 538 EWPMPEDLAEDDGEPEEGTSKDEGRASQEGPPGE 575
DB 541 EWPMPEDLAEDDGEPEEGTSKDEGRASQEGPPGE 578

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RESULT 14  
 ADN38411  
 ID ADN38411 standard; protein; 575 AA.

XX AC ADN38411;  
 XX DT 17-JUN-2004 (first entry)  
 XX

DE Novel human polynucleotide MO10b.

XX anti-HIV; cytostatic; antiarteriosclerotic; antidiabetic; antiasthmatic;  
 KW antiinflammatory; haemostatic; hypotensive; neuroprotective; anorectic;  
 KW nootropic; antidepressant; immunosuppressive; antibacterial; virucide;  
 KW fungicide; protozoacide; tranquilizer; anticonvulsant; osteopathic;  
 KW analgesic; antiparkinsonian; dermatological; antinfertility;  
 KW cardiomyopathy; atherosclerosis; diabetes; cell signal processing;  
 KW cerebroprotective; antiacladictive; MOIX-associated disorder;  
 KW metabolic pathway modulation; cancer; Von Hippel-Lindau syndrome;  
 KW Alzheimer's disease; stroke; tuberous sclerosis; hypercalcaemia;  
 KW Parkinson's disease; Huntington's disease; cerebral palsy; epilepsy;  
 KW Lesch-Nyhan syndrome; multiple sclerosis; ataxia-telangiectasia;  
 KW leukodystrophy; addiction; anxiety; depression; pain; obesity;  
 KW Crohn's disease; osteoporosis; inflammatory bowel disease; infertility;  
 KW hypertension; scleroderma; haemophilia; pancreatitis; autoimmune disease;  
 KW asthma; arthritis; immunodeficiency; HIV; infection;  
 KW graft-versus-host disease; gene therapy; vaccine; tissue typing;  
 KW pharmacogenomic; human.

XX Homo sapiens.

XX US2004029220-A1.

XX 12-FEB-2004.

XX 18-JUN-2002; 2002US-00174333.

XX 26-APR-2000; 2000US-0200158P.  
 XX 28-APR-2000; 2000US-0200613P.  
 XX 28-APR-2000; 2000US-0200780P.  
 XX 01-MAY-2000; 2000US-0201006P.  
 XX 01-MAY-2000; 2000US-0201007P.  
 XX 01-MAY-2000; 2000US-0201236P.  
 XX 01-MAY-2000; 2000US-0201238P.  
 XX 02-MAY-2000; 2000US-0201186P.  
 XX 03-MAY-2000; 2000US-0201474P.  
 XX 03-MAY-2000; 2000US-0201508P.  
 XX 25-JUL-2000; 2000US-0220591P.  
 XX 15-SEP-2000; 2000US-0232678P.  
 XX 22-JAN-2001; 2001US-0263217P.  
 XX 30-JAN-2001; 2001US-0265160P.  
 XX 16-FEB-2001; 2001US-0269531P.  
 XX 25-APR-2001; 2001US-00842758.  
 XX 18-JUN-2001; 2001US-0298994P.  
 XX 07-JUN-2002; 2002US-0386837P.

XX (VERN/) VERNET C A M.  
 PA (VERN/) FERNANDES E R.  
 PA (GERL/) GERLACH V.  
 PA (SHIM/) SHIMKETS R A.  
 PA (MALY/) MALYANKAR U M.  
 PA (BOLD/) BOLDOG F L.  
 PA (ZERR/) ZERRHUSEN B D.  
 PA (SPYT/) SPYTTER K A.  
 PA (MAUT/) MAUDMER K.  
 PA (TCH/) TCHERNYEV V T.  
 PA (PAD/) PADIGARU M.  
 PA (PAT/) PATTURAJAN M.  
 PA (BUR/) BURGESS C E.  
 PA (GANG/) GANGOLLI E A.  
 PA (SMIT/) SMITHSON G.  
 PA (RAST/) RASTELLI L.  
 PA (MACD/) MACDOUGALL J R.  
 PA (TAUP/) TAUPIER R J.  
 PA (GROS/) GROSSE W M.  
 PA (SZER/) SZEKRES E S.  
 PA (ALSO/) ALSOEROOK J P.  
 PA (ANDE/) ANDERSON D W.  
 PA (GUOX/) GUO X.  
 PA (LILL/) LI L.  
 PA (ZHON/) ZHONG M.





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OM protein - protein search, using sw model

Run on: February 10, 2005, 03:26:15 / Search time 27 Seconds  
(without alignment)  
1412.328 Million cell updates/sec

Title: US-09-927-267-1  
Perfect score: 2989  
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Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*  
  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1549.5	51.8	694	US-09-538-092-1351	Sequence 1351, Ap
2	1538.5	51.5	686	US-09-538-092-1037	Sequence 1037, Ap
3	1526.5	51.1	690	US-09-275-252A-19	Sequence 19, Appl
4	847	28.3	261	US-09-275-252A-18	Sequence 18, Appl
5	719	24.1	909	US-09-538-092-1315	Sequence 1315, Ap
6	488	16.3	129	US-08-997-685A-46	Sequence 46, Appl
7	475.5	15.9	126	US-08-997-685A-57	Sequence 57, Appl
8	468.5	15.7	126	US-08-997-685A-58	Sequence 58, Appl
9	466.5	15.6	528	US-08-997-685A-4	Sequence 4, Appl
10	457.5	15.3	504	US-09-086-436-33	Sequence 33, Appl
11	454.5	15.2	597	US-09-086-436-41	Sequence 41, Appl
12	450.5	15.1	597	US-08-997-685A-12	Sequence 12, Appl
13	441.5	14.8	749	US-08-997-685A-10	Sequence 10, Appl
14	441.5	14.8	710	US-09-086-436-39	Sequence 39, Appl
15	441.5	14.8	910	US-08-997-685A-2	Sequence 2, Appl
16	441.5	14.8	910	US-09-086-436-31	Sequence 31, Appl
17	421.5	14.1	506	US-09-086-436-35	Sequence 35, Appl
18	420.5	14.1	506	US-08-997-685A-6	Sequence 6, Appl
19	406	13.6	170	US-09-358-383C-27	Sequence 27, Appl
20	402	13.4	319	US-09-358-383C-22	Sequence 22, Appl
21	391	13.1	962	US-09-614-480-9	Sequence 9, Appl
22	391	13.1	962	US-09-694-777A-3	Sequence 3, Appl
23	391	13.1	962	US-10-422-075-9	Sequence 9, Appl
24	387.5	13.0	960	US-09-694-777A-21	Sequence 21, Appl
25	387.5	13.0	962	US-09-694-777A-24	Sequence 24, Appl
26	382.5	12.8	1284	US-09-343-494-9	Sequence 9, Appl
27	382.5	12.8	1284	US-09-358-383C-11	Sequence 11, Appl

28	380.5	12.7	989	US-09-694-777A-4	Sequence 4, Appl
29	380	12.7	1083	US-09-600-776-2	Sequence 2, Appl
30	380	12.7	1083	US-09-343-494-1	Sequence 1, Appl
31	379	12.7	1083	US-09-358-383C-2	Sequence 2, Appl
32	377	12.6	987	US-09-694-777A-22	Sequence 22, Appl
33	377	12.6	989	US-09-694-777A-23	Sequence 23, Appl
34	377	12.6	1082	US-09-336-643A-20	Sequence 20, Appl
35	376.5	12.6	988	US-09-614-480-2	Sequence 2, Appl
36	376.5	12.6	988	US-10-162-012-5	Sequence 5, Appl
37	376.5	12.6	988	US-10-422-075-2	Sequence 2, Appl
38	376.5	12.6	1107	US-09-358-383C-16	Sequence 16, Appl
39	375	12.5	1159	US-08-956-242-13	Sequence 13, Appl
40	375	12.5	1159	US-09-351-215-13	Sequence 13, Appl
41	375	12.5	1159	US-09-226-012-2	Sequence 2, Appl
42	375	12.5	1159	US-09-226-012-4	Sequence 4, Appl
43	375	12.5	1159	US-09-358-383C-10	Sequence 10, Appl
44	375	12.5	1159	US-09-275-252A-12	Sequence 12, Appl
45	370.5	12.4	888	US-08-956-242-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1									
US-09-538-092-1351									
; Sequence 1351, Application US/09538092									
; Patent No. 6753314									
; GENERAL INFORMATION:									
; APPLICANT: Glot, Joic									
; APPLICANT: Mansfield, Traci A.									
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same									
; FILE REFERENCE: 15966-542									
; CURRENT APPLICATION NUMBER: US/09/538, 092									
; PRIOR FILING DATE: 2000-03-29									
; PRIOR APPLICATION NUMBER: 60/127,352									
; PRIOR FILING DATE: 1999-04-01									
; PRIOR APPLICATION NUMBER: 60/178,965									
; PRIOR FILING DATE: 2000-02-01									
; NUMBER OF SEQ ID NOS: 1387									
; SOFTWARE: CuratPatSeqFormatter Version 0.9									
; SEQ ID NO 1351									
; LENGTH: 694									
; TYPE: PRT									
; ORGANISM: Homo sapiens									
; FEATURE:									
; NAME/KEY: misc_feature									
; LOCATION: (0)...(0)									
; OTHER INFORMATION: Polypeptide Accession Number Q16281									
US-09-538-092-1351									
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Matches 290; Conservative 112; Mismatches 140; Indels 9; Gaps 2									
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QY	129	VYRLGPHPTLRLNPLFAPRLFEAFDPTERTPAVPAFLAKMLYIFVVIHMSCLYF	188						
DB	263	YLVKVTNPEVRFNRLKFSRLFEFFDTRTKTNPNMFRIGNLVLIILIIHMACIYF	322						
QY	189	ALSRIGFGADAWVPDPAQGFERLIRQYLYSFSTLIITTVGDTPPPAREEYLFMV	248						
DB	323	ALSKRIGFGTDSWVYVNPISIPRHGLRSKRYISLWSTLTLITIGETPPVDEEYLFV	382						
QY	249	GDFLIANGFATIKWSMGSVYNNMTADAAPYPDHALYKRYMKLOHVRKLERRYITDYO	308						
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QY 309 HLQINKMTNEVAIIQHLPERLRAEVAVSVHLSTLSRVOIFONCEASILEELVLTQ 368  
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 QY 369 YSPREYVCRKGDIGQEMWIIIRREGOLAVVADGITOYAVLGAAGLYFGEISIIINIKGM 428  
 Db 503 FSPEDYVCRKGDIGQEMWIIIRREGOLAVVADGITOYAVLGAAGLYFGEISIIINIKGM 562  
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 Db 563 RRTANIKSLGSDLFCLSKEDLEVLSEYPOAQTIEMEKREIILKNKLDVNAEAEIA 621  
 QY 489 LQATSRRLGLDQDLDTQTKPARLLAELESSALKIAYRIERLEWOTR-----EWP 540  
 Db 622 DPEDEKREKQOLSSISDITQTRPARLLAEYNAQTOMKQKRLSQLESQVGGGDKPLADGE 681  
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 Db 682 VPGDATKTEBK 692

RESULT 2  
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 ; Sequence 1037, Application US/09538092  
 ; Patent No. 6753314  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Glot, Loic  
 ; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same  
 ; FILE REFERENCE: 15966-542  
 ; CURRENT APPLICATION NUMBER: US/09/538,092  
 ; PRIOR FILING DATE: 2000-03-29  
 ; PRIOR APPLICATION NUMBER: 60/127,352  
 ; PRIOR FILING DATE: 1999-04-01  
 ; PRIOR APPLICATION NUMBER: 60/178,965  
 ; NUMBER OF SEQ ID NOS: 1387  
 ; SOFTWARE: CuraPatSeqFormatter Version 0.9  
 ; SEQ ID NO 1037  
 ; LENGTH: 686  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (0)..(0)  
 ; OTHER INFORMATION: Polypeptide Accession Number P23973  
 US-09-538-092-1037

Query Match 51.5%; Score 1538.5; DB 4; Length 686;  
 Best Local Similarity 54.0%; Pred. No. 1.4e-146;  
 Matches 285; Conservative 113; Mismatches 129; Indels 1; Gaps 1;  
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 QY 66 LVAMLVLDYTSDLVLYLDVNVRFHGFLEQGLVVDKGRISRRYRTMSFFDLASLMP 125  
 Db 193 LEVWLLIDVSDIYLLIDMFVTRTGYLEQGLVKEELKINKKSNLQFKLDVLSLPT 252  
 QY 126 DVVYVRLGPHPTPLRLNRLRLRFLAPRLFEAFDRTETRTAYPNAFRIAKMLYIFVVIHNSC 185  
 Db 253 DLVLFKGMWYPEIRLNLRLRFSRMFEFQRTETRTAYPNIIRISNLVMTIIVIIHNNAC 312  
 QY 186 LVFALSRVYGRDAMVYVDPDPAQGFERLROYLYSFYSTLIITVGDTPPAREEYL 245  
 Db 313 VFVSIISAKGFNDTWYVPDINDPEFGLARKYVSLYWSLTLLTITIGETPPVDRSEYV 372  
 QY 246 FVWGFLLAVMGFATIGMSMSVLYNNMTADAAPYDPHALVKKYMKLOHNRKLEERYD 305  
 Db 373 FVVVDFLLIGVLIFFATIVGNISMSNNNAABAFQARIDAIKOYMFRRVSKMEKRVIK 432

QY 306 WYQHLQINKMTNEVAIIQHLPERLRAEVAVSVHLSTLSRVOIFONCEASILEELVLTQ 365  
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 QY 366 POTYSPGEVYCRKGDIGQEMWIIIRREGOLAVVADGITOYAVLGAAGLYFGEISIIINIKGM 425  
 Db 493 POTYSPGEVYCRKGDIGQEMWIIIRREGOLAVVADGITOYAVLGAAGLYFGEISIIINIKGM 552  
 QY 426 SGNRTANIKSLGSDLFCLSKEDLEVLSEYPOAQTIEMEKREIILKNKLDVNAEAEIA 485  
 Db 553 AGNRTANIKSLGSDLFCLSKEDLEVLSEYPOAQTIEMEKREIILKNKLDVNAEAEIA 612  
 QY 486 EIALQATSRRLGLDQDLDTQTKPARLLAELESSALKIAYRIERLE 533  
 Db 613 GSDPD-LKEKVTREKSDVLDLQTRPARLLAEYSEMOCKLQRLTKY 659

RESULT 3  
 US-09-275-252A-19  
 ; Sequence 19, Application US/09275252A  
 ; Patent No. 6641997  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MacKinnon, Roderick  
 ; TITLE OF INVENTION: The Rockefeller University  
 ; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With  
 ; TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation  
 ; FILE REFERENCE: 018512-00290105  
 ; CURRENT APPLICATION NUMBER: US/09/275,252A  
 ; PRIOR FILING DATE: 1999-03-24  
 ; PRIOR APPLICATION NUMBER: US 09/045,529  
 ; PRIOR FILING DATE: 1998-03-20  
 ; PRIOR APPLICATION NUMBER: US 09/054,347  
 ; PRIOR FILING DATE: 1998-04-02  
 ; PRIOR APPLICATION NUMBER: WO PCT/US99/06307  
 ; PRIOR FILING DATE: 1999-03-22  
 ; NUMBER OF SEQ ID NOS: 42  
 ; SOFTWARE: Patentin Ver. 2.1  
 ; SEQ ID NO 19  
 ; LENGTH: 690  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-275-252A-19

Query Match 51.1%; Score 1526.5; DB 4; Length 690;  
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 QY 186 LVFALSRVYGRDAMVYVDPDPAQGFERLROYLYSFYSTLIITVGDTPPAREEYL 245  
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 Db 377 FVVVDFLLIGVLIFFATIVGNISMSNNNAABAFQARIDAIKOYMFRRVSKMEKRVIK 436  
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 Db 437 WEDYLMTKKTVDEKEVLYKLPDKLRARIAINVHDLTKKRIFFADCGAGLLVELVLTQ 496  
 QY 366 POTYSPGEVYCRKGDIGQEMWIIIRREGOLAVVADGITOYAVLGAAGLYFGEISIIINIKGM 425

AFFILIATION: THE LIBRARY OF CONGRESS UNIVERSITY

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; APPLICANT: Kandel, Eric
; TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof
; FILE REFERENCE: 0575/54806
; CURRENT APPLICATION NUMBER: US/08/997,685A
; CURRENT FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
; LENGTH: 129
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US-08-997-685A-46

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Query Match
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Matches 92; Conservative 20; Mismatches 17; Indels 0; Gaps 0;

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   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 416 ISIIINIKGNMGNRRRTANIKSLIGSDLPFCLSKEDLREVLSEYPOAQTIIMEKREILL 475
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ISIIINIKGNMGNRRRTANIKSLIGSDLPFCLSKEDLREVLSEYPOAQTIIMEKREILL 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 476 NKLDVNAEA 484
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 GLLDENEVA 129
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

```

RESULT 7
US-08-997-685A-57
; Sequence 57, Application US/08997685A
; Patent No. 6551821
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University
; TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof
; FILE REFERENCE: 0575/54806
; CURRENT APPLICATION NUMBER: US/08/997,685A
; CURRENT FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57
; LENGTH: 126
; TYPE: PRT
; ORGANISM: bovine;
; FEATURE:
; NAME/KEY: NON CONS
; LOCATION: (47)..(48)
; OTHER INFORMATION: gap in alignment
; FEATURE:
; NAME/KEY: NON CONS
; LOCATION: (56)..(57)
; OTHER INFORMATION: gap in alignment
US-08-997-685A-57

```

```

Query Match
Best Local Similarity 15.9%; Score 475.5; DB 4; Length 126;
Matches 91; Conservative 20; Mismatches 15; Indels 1; Gaps 1;

```

```

QY 354 ASLLEELVLTLPQPTYSPEYVCRKGDIGQEMTIRREGQLAVVADDTGYAVLGAAGLYF 413
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 ASLLELVLTLPQPTYS- GDYICRKGDDIGREMYIIKEGKLAVVADDTGYAVLGAAGLYF 59
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 414 GEISIIINIKGNMGNRRRTANIKSLIGSDLPFCLSKEDLREVLSEYPOAQTIIMEKREILL 473
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 60 GEISIIINIKGNMGNRRRTANIKSLIGSDLPFCLSKEDLREVLSEYPOAQTIIMEKREILL 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 474 KMKLDV 480
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 120 KQGLLDI 126
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

```

RESULT 8
US-08-997-685A-58
; Sequence 58, Application US/08997685A
; Patent No. 6551821
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University
; TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof
; FILE REFERENCE: 0575/54806
; CURRENT APPLICATION NUMBER: US/08/997,685A
; CURRENT FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 126
; TYPE: PRT
; ORGANISM: catfish;
; FEATURE:
; NAME/KEY: NON CONS
; LOCATION: (7)..(8)
; OTHER INFORMATION: gap in alignment
; FEATURE:
; NAME/KEY: NON CONS
; LOCATION: (47)..(48)
; OTHER INFORMATION: gap in alignment
; FEATURE:
; NAME/KEY: NON CONS
; LOCATION: (56)..(57)
; OTHER INFORMATION: gap in alignment
; FEATURE:
; NAME/KEY: NON CONS
; LOCATION: (66)..(67)
; OTHER INFORMATION: gap in alignment
US-08-997-685A-58

```

```

Query Match
Best Local Similarity 15.7%; Score 468.5; DB 4; Length 126;
Matches 90; Conservative 19; Mismatches 16; Indels 1; Gaps 1;
QY 354 ASLLEELVLTLPQPTYSPEYVCRKGDIGQEMTIRREGQLAVVADDTGYAVLGAAGLYF 413
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 ASLLELVLTLPQPTYS- GDYICRKGDDIGREMYIIKEGKLAVVADDTGYAVLGAAGLYF 59
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 414 GEISIIINIKGNMGNRRRTANIKSLIGSDLPFCLSKEDLREVLSEYPOAQTIIMEKREILL 473
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 60 GEISIIINIKGNMGNRRRTANIKSLIGSDLPFCLSKEDLREVLSEYPOAQTIIMEKREILL 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 474 KMKLDV 480
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 120 KQGLLDI 126
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

```

RESULT 9
US-08-997-685A-4
; Sequence 4, Application US/08997685A
; Patent No. 6551821
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University
; TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof

```



```

; FILE REFERENCE: 0575/54806
; CURRENT APPLICATION NUMBER: US/08/997,685A
; CURRENT FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 528
; TYPE: PRT
; ORGANISM: mouse;
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AAC40125
; DATABASE ENTRY DATE: 1998-05-29
; RELEVANT RESIDUES: (1)..(504)
US-08-997-685A-4

```

```

Query Match      15.6%; Score 466.5; DB 4; Length 528;
Best Local Similarity 25.3%; Pred. No. 4,3e-38;
Matches 122; Conservative 109; Mismatches 202; Indels 49; Gaps 12;

```

```

QY 26 VLDPSGDYVWMLNTWPFVWVNYLIIIVCRACFPDLQHGVLVAVLVLDYSDLYLDMV 85
DB 27 IHPYSDRFYWDFTMLFMVGNLIIIVGITE--FKDETTAPWIVFVNSDTPFLMDLV 84
QY 86 VRFHTGFL--EGGILVVDKGRISRYVTVTSFELDLASIMPDVVY-----129
DB 85 INFRTGIVIEDTEIILDEPKIKKKYLRW--FVDFVSSIPVDYFLIVEKGIDSEVYKT 143
QY 130 ---VRLGHTPTLRNLNRLRPLRPLRPLRPLRPLRPLRPLRPLRPLRPLRPLRPLR 181
DB 144 ARLRIVFTKILSLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRL 203
QY 182 WNSCLYFALSRYLGFGRDAWVYPPDAPGPFERLRQY--LYSF---YFSTLILTTVGD 235
DB 204 WDGCLOFLVPMLODPSPDCWVSN-----NMVNSWSELVSFALFKAMSHMLCIGYGRQ 257
QY 236 PPPAREEYLFWVGDFFLAVMGFATMGSMSSVYNNMTADAFYPDHALVKKYKLOHV 295
DB 258 APESMTDITLWML--SMIVGATCYAMFIGHATLQSLDSRRQYQYQYQYQYQYQYQY 316
QY 296 NKLERRVYIDWYQHLQINKMTNEVALIQLPERLRAEVAVSMLSTRVOIFONCEAS 355
DB 317 PADFRQKIHDIYEH--RYQGRKMSDEDSILGELNGPLREIIVNCRKRLVSMPLFANADPN 375
QY 356 LLEBLVLYLQPTYSRGEVYCKDIOGEMTIIREGOLAVVADDITQYAVLAGLYRGE 415
DB 376 FYTAMLTCLKFVFPQGDYIIRGGTIGKKMYFIQHGVSVLTKG--NKEMKLSDSYRGE 433
QY 416 ISIIINKGMSGNRRITANKISLGYSDLFCLSKEDLREVLSEYPOAOTIMEEKGREILK 475
DB 434 ICL-----LTRGRITASVRADTYCRLYSLVDNFEVLEETPMRRAFETVAIDRLRI 487
QY 476 NK 477
DB 488 GK 489

```

```

RESULT 10
US-09-086-436-33
; Sequence 33, Application US/09086436
; Patent No. 6703485
; GENERAL INFORMATION:
; APPLICANT: Kandel, Eric R.
; APPLICANT: Santoro, Bina
; APPLICANT: Bartsch, Dusan
; APPLICANT: Siegelbaum, Steven
; APPLICANT: Tibbs, Garech
; APPLICANT: Grant, Seth
; TITLE OF INVENTION: Brain or Heart Cyclic Nucleotide Gated Ion Channel and
; TITLE OF INVENTION: Uses thereof
; FILE REFERENCE: 0575/54806-A
; CURRENT APPLICATION NUMBER: US/09/086,436
; CURRENT FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 67

```

```

; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 33
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Murine
US-09-086-436-33

```

```

Query Match      15.3%; Score 457.5; DB 4; Length 504;
Best Local Similarity 25.1%; Pred. No. 3,3e-37;
Matches 121; Conservative 109; Mismatches 203; Indels 49; Gaps 12;

```

```

QY 26 VLDPSGDYVWMLNTWPFVWVNYLIIIVCRACFPDLQHGVLVAVLVLDYSDLYLDMV 85
DB 27 IHPYSDRFYWDFTMLFMVGNLIIIVGITE--FKDETTAPWIVFVNSDTPFLMDLV 84
QY 86 VRFHTGFL--EGGILVVDKGRISRYVTVTSFELDLASIMPDVVY-----129
DB 85 INFRTGIVIEDTEIILDEPKIKKKYLRW--FVDFVSSIPVDYFLIVEKGIDSEVYKT 143
QY 130 ---VRLGHTPTLRNLNRLRPLRPLRPLRPLRPLRPLRPLRPLRPLRPLRPLRPLR 181
DB 144 ARLRIVFTKILSLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRL 203
QY 182 WNSCLYFALSRYLGFGRDAWVYPPDAPGPFERLRQY--LYSF---YFSTLILTTVGD 235
DB 204 WDGCLOFLVPMLODPSPDCWVSN-----NMVNSWSELVSFALFKAMSHMLCIGYGRQ 257
QY 236 PPPAREEYLFWVGDFFLAVMGFATMGSMSSVYNNMTADAFYPDHALVKKYKLOHV 295
DB 258 APESMTDITLWML--SMIVGATCYAMFIGHATLQSLDSRRQYQYQYQYQYQYQY 316
QY 296 NKLERRVYIDWYQHLQINKMTNEVALIQLPERLRAEVAVSMLSTRVOIFONCEAS 355
DB 317 PADFRQKIHDIYEH--RYQGRKMSDEDSILGELNGPLREIIVNCRKRLVSMPLFANADPN 375
QY 356 LLEBLVLYLQPTYSRGEVYCKDIOGEMTIIREGOLAVVADDITQYAVLAGLYRGE 415
DB 376 FYTAMLTCLKFVFPQGDYIIRGGTIGKKMYFIQHGVSVLTKG--NKEMKLSDSYRGE 433
QY 416 ISIIINKGMSGNRRITANKISLGYSDLFCLSKEDLREVLSEYPOAOTIMEEKGREILK 475
DB 434 ICL-----LTRGRITASVRADTYCRLYSLVDNFEVLEETPMRRAFETVAIDRLRI 487
QY 476 NK 477
DB 488 GK 489

```

```

RESULT 11
US-09-086-436-41
; Sequence 41, Application US/09086436
; Patent No. 6703485
; GENERAL INFORMATION:
; APPLICANT: Kandel, Eric R.
; APPLICANT: Santoro, Bina
; APPLICANT: Bartsch, Dusan
; APPLICANT: Siegelbaum, Steven
; APPLICANT: Tibbs, Garech
; APPLICANT: Grant, Seth
; TITLE OF INVENTION: Brain or Heart Cyclic Nucleotide Gated Ion Channel and
; TITLE OF INVENTION: Uses thereof
; FILE REFERENCE: 0575/54806-A
; CURRENT APPLICATION NUMBER: US/09/086,436
; CURRENT FILING DATE: 1998-05-28
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 41
; LENGTH: 597
; TYPE: PRT
; ORGANISM: Human
US-09-086-436-41

```

```

Query Match      15.2%; Score 454.5; DB 4; Length 597;

```



```

QY  PPARBEEYLFMYDVFLLAWGFATIMGSSVIYMMNTADAFAFYDHALYCKKQJLQHN 236
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  237 PPMSDMLITML-SMIVGATCYAMVGVGATALIGLDBSSRQCYEKYQYQGYMSFHKLP 303
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  245 KLEERVIVMYOHLQINKKMTNEVALIOLHPERLPAEVAASVHLSSTLSRVOIFONCEASTL 356
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  297 RLEERVIVMYOHLQINKKMTNEVALIOLHPERLPAEVAASVHLSSTLSRVOIFONCEASTL 356
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  304 ADMROKIHUYEH-RQGGKI PDEENILMETLNDPLREEIVNFCRKLVAWMLP.FMNAIDPNF 362
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  357 LEEIYV.LKLOPOTFSPSEYVCRKGDJGOEYV.IIIRGQLVAVDDGITQAVLGAALYGEI 416
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  363 VTMLSLKRFVYQPDYIIRGAVGKKMYFIQHGVAQVITKS--SKMKLTDGSIYGEI 420
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  417 SIINIKGNMSGNRRNTANIKSLGYSDL.FCLSKEDLEVLSEYPOAQITME----- 466
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  421 CLLT-KG-----RTASVADTYCRSLYSVDNFNEVLEEYPMRRAPETVAIDRLDRIG 474
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  467 KGREIILLKXNKLDVYN 481
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  475 KKNISILQKFOKDNL 489
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 14
US-09-086-436-39
: Sequence 39, Application US/09086436
: Patent No. 6703485
: GENERAL INFORMATION:
: APPLICANT: Kandell, Eric R.
: APPLICANT: Santoro, Bina
: APPLICANT: Bartsch, Dusan
: APPLICANT: Siegelbaum, Steven
: APPLICANT: Tibbs, Gareth
: APPLICANT: Grant, Seth
: TITLE OR INVENTION: Brain or Heart Cyclic Nucleotide Gated Ion Channel and
: TITLE OR INVENTION: Uses Thereof
: FILE REFERENCE: 0575/54806-A
: CURRENT APPLICATION NUMBER: US/09/086,436
: NUMBER OF SEQ ID NOS: 67
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 39
: LENGTH: 749
: TYPE: PRT
: ORGANISM: Human
: US-09-086-436-39

```

[illegible]

```

QY 357 IEEIYKULQRYSPSEYVCRKGDIGQSMYIIRREGQLAVNADGGITQYAVGAGLYGEI 416
Dh 363 VYAMSEKLEPVPQEDYIIRGGAAGKMYIIOGVAGVITYS--SYEMKLTDSGYEII 420
QY 417 SIINIKGNNSGNRRPTANIKSLGYSDLPFCISKEDLREVLSEYPOAQTIMEE----- 466
Dh 421 CLIT-KG-----RRDASVADYTCYKLSLVDFNEVLEETPMRRAPETVAIDRLDRIG 474
QY 467 KGREILLKNNKLDVN 481
Dh 475 KKNISILLQKFQKDLN 489

```

```

: RESULT 15
: US-08-997-685A-2
: Sequence 2, Application US/08997685A
: Patent No. 6551821
:
: GENERAL INFORMATION:
:
: APPLICANT: The Trustees of Columbia University
: APPLICANT: Kandell, Eric
: TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof
: FILE REFERENCE: 0575/54806
: CURRENT APPLICATION NUMBER: US/08/997,685A
: CURRENT FILING DATE: 1997-12-12
:
: NUMBER OF SEQ ID NOS: 60
:
: SOFTWARE: PatentIn version 3.1
:
: SEQ ID NO 2

```

```

NAME/KEY: DOMAIN
LOCATION: (130)..(148)
OTHER INFORMATION: S1
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (164)..(185)
OTHER INFORMATION: S2
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (208)..(229)
OTHER INFORMATION: S3
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (243)..(271)
OTHER INFORMATION: S4
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (291)..(313)
OTHER INFORMATION: S5
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (332)..(358)
OTHER INFORMATION: P
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (367)..(387)
OTHER INFORMATION: S6
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (472)..(602)
OTHER INFORMATION: CNB
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AAC53518
DATABASE ENTRY DATE: 1997-12-27
RELEVANT RESIDUES: (1)..(910)

```

Query Match 14.8%; Score 441.5; DB 4; Length 910;  
Best Local Similarity 24.2%; Pred. No. 3.7e-35;  
Matches 120; Conservative 116; Mismatches 202; Indels 57; Gaps 15;

```

Oy 26 VLDPGSDYYWMLNTMFPVWMLIIIVCRACFPDIQHGVLAVMLVDYSDLYLDMV 85
Db 123 IIPHSDFRFFYDMLIMIMVGNLVIIIPVGITF--FTGQTTPIIFNVASDPTVFLDLII 180
Oy 86 VRPHTGFL-EOGIIIVDKRISRRYRTWSPFLDLASIMPTDVY-----129
Db 181 MNFRGTVNEDESEIILDPKVIKNMYLKSWM-FVVDFISSIPVDYIFLIVEKGMDESVYKT 239
Oy 130 ---VLSGHTPTLRNRFRLRAPRLF-----EAFDRF-ETRTAEPNAPRIAKMLYIFV 178
Db 240 ARALKIVRFTKLISLRILRLIRYIHQWEIIFHMTYDLASAVARIIFNLIGMML--L 296
Oy 179 VIHMNSCLYFALSRYLGFGRDAMVYPDPAPGFERLRROYLSFY--FSTLILTTVGDP 236
Db 297 LCHWDGCIQFLVPLIQDFPPDCWGLN--EMVNDSWGKQYSYALFKAMSHMLCIGYGAQA 354
Oy 237 PPAREEYLFVVGDFLLAVMGFATIMGSNSVIYMMNTADAAFYDPHALVKKYMKLQHVN 296
Db 355 FVMSMDLWITML-SMIVGATCYAMFVGHATALIQSLDSSRRQYQEKYQVEQYMSFHKLP 413
Oy 297 RKLERRVIDWYOHQIINKKMTNEVALQHLPERLRBAVAVSVHLSTLSRVOIFQNCESL 356
Db 414 ADMROKIHDIYEH-RYQGIIFDENILSELNDPLREBIVNEVCRLVAMPLFANADPNF 472
Oy 357 LEEVLVTLQOPQYSPGEYVCRKGDIGOEMYIIREGQLAVVADGITOYAVLGAGLYFGEI 416
Db 473 VTAMLSKLRFEVFGQDVIIRREGAVGKMYFIQHGVAGVITKS--SKEMKLTDSYFGEI 530
Oy 417 SIINIKGMMSGNRRTANIKSLGYSDFCLSKEDLREVLSEYPOAQTIME-----466
Db 531 CLLT-KG----RRTASVRADYCRLYSLYSVDNFNEVLSEYPMRRARAFETVAIDRLDRIG 584
Oy 467 KGREILKMNKLDVN 481
Db 585 KKNSTILQKFQKDLN 599

```

Search completed: February 10, 2005, 03:45:00  
 Job time : 28 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 9, 2005, 20:51:50 ; Search time 111 Seconds

(without alignments)  
2980.544 Million cell updates/sec

Title: US-09-927-267-1

Perfect score: 2989

Sequence: 1 MSQDKVKTSTSSPPAPSKA.....EGTSKDEGRASQEGPPGPE 575

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: UniProt\_02.\*

1: uniprot\_prot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2811	94.0	575	1 CNGX_RAT	064359 ractus novy
2	2118	70.9	474	2 O81V77	081v77 homo sapien
3	1638.5	54.8	609	2 O8JFP0	08jfp0 ictalurus p
4	1585.5	53.0	551	2 O8JFN9	08jfn9 ictalurus p
5	1582.5	52.9	631	2 O8CFV6	08cfv6 mus musculu
6	1579	52.8	706	1 CNG3_BOVIN	029441 bos taurus
7	1578	52.8	611	2 O9QW7	09qwm7 ractus novy
8	1578	52.8	632	2 O9ER32	09er32 ractus novy
9	1578	52.8	670	2 O9ER33	09er33 ractus novy
10	1573.5	52.6	631	1 CNG3_MOUSE	09jiz8 mus musculu
11	1568	52.5	663	1 CNG2_BOVIN	003041 bos taurus
12	1562.5	52.3	735	1 CNG1_CHICK	090805 gallus gall
13	1562	52.3	664	1 CNG2_BABIT	028718 oryctolagus
14	1558	52.1	664	1 CNG2_RAT	000195 ractus novy
15	1558	52.1	664	1 O8OXH6	08oxh6 mus musculu
16	1558	52.1	664	2 AAD41473	Aad41473 ractus no
17	1549.5	51.8	694	1 CNG3_HUMAN	016681 homo sapien
18	1547	51.8	664	1 CNG2_MOUSE	062198 mus musculu
19	1544.5	51.7	690	1 CNG1_BOVIN	000194 b cgmpp-gate
20	1544.5	51.7	698	2 O6ZNA7	06zna7 homo sapien
21	1544.5	51.7	698	2 BADI8468	Badi8468 homo sapi
22	1538.5	51.5	686	1 CNG1_HUMAN	P29973 h cgmpp-gate
23	1538.5	51.5	686	2 O9N0H4	O9n0h4 sus scrofa
24	1533.5	51.3	684	1 CNG1_MOUSE	P29974 m cgmpp-gate
25	1532.5	51.3	691	1 CNG1_CANFA	Q28279 c cgmpp-gate
26	1532	51.3	683	1 CNG1_RAT	Q62827 r cgmpp-gate
27	1529	51.2	645	1 CNG3_CHICK	090980 gallus gall
28	1519.5	50.8	637	2 O804I6	O804i6 catarrhini a
29	1436.5	48.1	682	1 CNG_ICPNU	P55534 ictalurus p
30	1378.5	46.1	737	2 O8UVT8	O8uvt8 oncorhynch
31	1244.5	41.6	586	2 O7PW88	O7pw88 anopheles g

32	1235	41.3	665	1 CNG_DROME	Q24278 drosophila
33	1119.5	37.5	733	1 CNG_CABEL	Q03611 caenorhabd
34	993	33.2	1218	2 O9WZ01	O9wz01 drosophila
35	990.5	33.1	900	2 O97119	O97119 limulus pol
36	990	33.1	799	2 O7PTE6	O7pte6 anopheles g
37	922	30.8	189	2 O6Q214	O6q214 ractus novy
38	922	30.8	189	2 AAS87325	Aas87325 ractus no
39	920	30.8	189	2 O6Q213	O6q213 mus musculu
40	920	30.8	189	2 AAS87326	Aas87326 mus muscu
41	881.5	29.5	1126	2 O7Q9A9	O7q9a9 anopheles g
42	879	29.4	1453	2 O8IR35	O8ir35 drosophila
43	879	29.4	1453	2 AAN09666	Aan09666 drosophila
44	879	29.4	1463	2 O9U5E2	O9u5e2 drosophila
45	879	29.4	1853	2 O9VXV8	O9vxv8 drosophila

## ALIGNMENTS

RESULT 1  
CNGX\_RAT STANDARD; PRT; 575 AA.

AC 064359;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 29-MAR-2004 (Rel. 43, Last annotation update)  
DE Cyclic-nucleotide-gated olfactory channel OCN2 subunit.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_Taxid=10116;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley;  
RX MEDLINE=9437458; PubMed=7522325;  
RA Bradley J., Li J., Davidson N., Lester H.A., Zinn K.;  
RT "Heteromeric olfactory cyclic nucleotide-gated channels: a subunit  
that confers increased sensitivity to cAMP."  
RL Proc. Natl. Acad. Sci. U.S.A. 91:8890-8894(1994).  
RN (2)  
RP SEQUENCE FROM N.A.  
RC TISSUE=Olfactory neuroepithelium;  
RX MEDLINE=9500063; PubMed=7522482;  
RA Liman E.R., Buck L.B.;  
RT "A second subunit of the olfactory cyclic nucleotide-gated channel  
confers high sensitivity to cAMP."  
RL Neuron 13:611-621(1994).  
RN (3)  
RP SEQUENCE OF 7-35 FROM N.A.  
RC STRAIN=Sprague-Dawley;  
RA Bradley J., Zhang Y., Bakin R., Lester H.A., Ronnett G., Zinn K.;  
RT Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Odorant signal transduction is probably mediated by a G-  
protein coupled cascade using cAMP as second messenger. The  
olfactory channel can be shown to be activated by cyclic  
nucleotides which leads to a depolarization of olfactory sensory  
neurons.  
CC -!- SUBUNIT: Heterooligomer of OCN1 and OCN2 subunits.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- TISSUE SPECIFICITY: Olfactory neurons.  
CC -!- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel  
(TC 1.A.1.5) family.  
CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC EMBL, U12623; AAA21464.1; -

[illegible]

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Db      158  ILDMVVRFHFTGLEGILVVDKGRISRRYRTWSPFLDLASIMPTDVVYRLGPHPTLR
Qy      200  LNRPLRAREPAREPRTERTRTAYPNARFAXMLYFYVYIHNSCLYFALSRYLGGRDA
Db      218  LNRFRAPPLFAFRTERTRTAYPNARFAXMLYFYVYIHNSCLYFALSRYLGGRDA
Qy      260  WYPPPAQGFRLRRQYLYSFYFSTLITTTGDTPPPARBEEYLFVMDFFLAVMGFAT
Db      278  WYPPPAQGFRLRRQYLYSFYFSTLITTTGDTPPPARBEEYLFVMDFFLAVMGFAT
Qy      320  IMSGSSVYLYNNMTADAFYPDHALVKKYMKLOHVNKLERVYDWOHLQINKKMTNEV
Db      338  IMSGSSVYLYNNMTADAFYPDHALVKKYMKLOHVNKLERVYDWOHLQINKKMTNEV
Qy      380  ALLOHLPRLRAEVAVSHLSTLSRVQIFONCEASLLEELVLTLOPQYSPGECYCRKD
Db      398  ALLOHLPRLRAEVAVSHLSTLSRVQIFONCEASLLEELVLTLOPQYSPGECYCRKD
Qy      423  IGOEWYIIRREGOLAVVADDDGTQYAVLAGAGLYFGEISINIKG
Db      441  IGOEWYIIRREGOLAVVADDDGTQYAVLAGAGLYFGEISINIKG

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## RESULT 3

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ID      609 AA.  PRELIMINARY;  PRT;  609 AA.
AC      08JFN9;
DT      01-OCT-2002 (TREMBlrel. 22, Created)
DT      01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DE      01-MAR-2004 (TREMBlrel. 26, Last annotation update)
GN      Cyclic nucleotide-gated channel modulatory subunit CNCA4a.
GN      Name=CNCA4;
OS      Ictalurus punctatus (Channel catfish).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC      Ictaluridae; Ictalurus.
OX      NCBI_TaxID=7998;
RN      [1]
RP      TISSUE=olfactory neuroepithelium;
RC      YAO H., Vosseshail L.B., Tibbs G.R., Sun Z.-P., Young E.C.,
RA      Siegelbaum S.A.;
RL      Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR      GO:GO:0016021; C:integral to membrane; IEA.
DR      GO:GO:0005216; F:pilocarpine channel activity; IEA.
DR      GO:GO:0005267; F:pilocarpine channel activity; IEA.
DR      GO:GO:0006811; P:ion transport; IEA.
DR      GO:GO:0006813; P:pilocarpine ion transport; IEA.
DR      InterPro: IPR000595; CNMP binding.
DR      InterPro: IPR005821; Ion trans.
DR      InterPro: IPR001622; K+channel_pore.
DR      Pfam: PF00027; CNMP_binding; 1.
DR      SMART: SM00100; CNMP; 1.
DR      PROSITE: PS00888; CNMP_BINDING_1; UNKNOWN_1.
DR      PROSITE: PS00889; CNMP_BINDING_2; 1.
DR      PROSITE: PS00442; CNMP_BINDING_3; 1.
KW      Ion transport; Ionic channel; Transmembrane; Transport.
SQ      SEQUENCE 609 AA; 70313 MW; 5C01AE4B3AB64D24 CRC64;

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Query Match 54.8%; Score 1638.5; DB 2; Length 609;

Best Local Similarity 55.5%; Pred. No. 2.2e-102; Matches 312; Conservative 94; Mismatches 139; Indels 17; Gaps 4;

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Qy      85  VLDPSGDYVYVMTVFPVYVNLILVGRACPPDLQHGVLVAVLVDYTSDDLVLVDV
Db      103  VLDPSGDYVYVMTVFPVYVNLILVGRACPPDLQHGVLVAVLVDYTSDDLVLVDV
Qy      145  VERHFGFLVGGILVVDKGRISRRYRTWSPFLDLASIMPTDVVYRLGPHPTLR
Db      163  IVRVGTGYLEOGSLVRDMSRLKKRYLHSSQFLDLVLSQFLPTDLLVSDPFTVVRINRFL

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Qy      205  RAPRLFEAFDRTERTRTAYPNARFAXMLYFYVYIHNSCLYFALSRYLGGRDAWYVD
Db      223  RSPRLSEALERETRTAYPNARFAXMLYFYVYIHNSCLYFALSRYLGGRDAWYVD
Qy      265  PAQGFRLRRQYLYSFYFSTLITTTGDTPPPARBEEYLFVMDFFLAVMGFATMSGM
Db      283  TTDIEENSTRQYLYSFYFSTLITTTGDTPPPARBEEYLFVMDFFLAVMGFATMSGM
Qy      325  SSIVYNNMTADAFYPDHALVKKYMKLOHVNKLERVYDWOHLQINKKMTNEVALH
Db      343  GSIVYNNMTADAFYPDHALVKKYMKLOHVNKLERVYDWOHLQINKKMTNEVALH
Qy      385  LPERLRAEVAVSHLSTLSRVQIFONCEASLLEELVLTLOPQYSPGECYCRKDGOEM
Db      403  LPERLRAEVAVSHLSTLSRVQIFONCEASLLEELVLTLOPQYSPGECYCRKDGOEM
Qy      445  YIIRREGOLAVVADDDGTQYAVLAGAGLYFGEISINIKGMSGNRTANIKSLGSPFLC
Db      463  YIIRREGOLAVVADDDGTQYAVLAGAGLYFGEISINIKGMSGNRTANIKSLGSPFLC
Qy      505  SKEDLREVSEYPOAQTIWEKGRRLKMKLVNVAABEIALOATESRLRGDQOLD
Db      521  SKEDLREVSEYPOAQTIWEKGRRLKMKLVNVAABEIALOATESRLRGDQOLD
Qy      555  DIQTKFARILAESSALKIAYRIERLEWQTEWMPEDL-----AEADDEGEPD-----
Db      578  DIQTKFARILAESSALKIAYRIERLEWQTEWMPEDL-----AEADDEGEPD-----
Qy      575  --EGTSKDEGRASQGPPE
Db      600  DEGEQEEERPOEERGDGEE

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## RESULT 4

```

ID      551 AA.  PRELIMINARY;  PRT;  551 AA.
AC      08JFN9;
DT      01-OCT-2002 (TREMBlrel. 22, Created)
DT      01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DE      01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE      Cyclic nucleotide-gated channel modulatory subunit CNCA4b truncated isoform.
GN      Name=CNCA4;
OS      Ictalurus punctatus (Channel catfish).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC      Ictaluridae; Ictalurus.
OX      NCBI_TaxID=7998;
RN      [1]
RP      TISSUE=olfactory neuroepithelium;
RC      YAO H., Vosseshail L.B., Tibbs G.R., Sun Z.-P., Young E.C.,
RA      Siegelbaum S.A.;
RL      Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR      EMBL: AF522298; AAM70510.1; -.
DR      GO:GO:0016021; C:integral to membrane; IEA.
DR      GO:GO:0005216; F:pilocarpine channel activity; IEA.
DR      GO:GO:0005267; F:pilocarpine channel activity; IEA.
DR      GO:GO:0006811; P:ion transport; IEA.
DR      GO:GO:0006813; P:pilocarpine ion transport; IEA.
DR      InterPro: IPR000595; CNMP binding.
DR      InterPro: IPR005821; Ion trans.
DR      InterPro: IPR001622; K+channel_pore.
DR      Pfam: PF00027; CNMP_binding; 1.
DR      SMART: SM00100; CNMP; 1.
DR      PROSITE: PS00888; CNMP_BINDING_1; UNKNOWN_1.
DR      PROSITE: PS00889; CNMP_BINDING_2; 1.
DR      PROSITE: PS00442; CNMP_BINDING_3; 1.
KW      Ion transport; Ionic channel; Transmembrane; Transport.
SQ      SEQUENCE 551 AA; 63371 MW; 8C51F06B8854580D CRC64;

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Query Match 53.0%; Score 1585.5; DB 2; Length 551;

Best Local Similarity 55.6%; Pred. No. 7.4e-99;  
Matches 304; Conservative 91; Mismatches 135; Indels 17; Gaps 4;

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QY 41 MWFPMVNYLIIIVRACRPPDQHGIVLAVLVDTSDLLVLDVVRVFRHTGFEQGLIV 100
Db 1 MWFPMVNYLIIIVRACRPPDQHGIVLAVLVDTSDLLVLDVVRVFRHTGFEQGLIV 100
QY 101 DKGISRRYVWTWSPFLDLASLMPDVTDVYVRLGPHPTLRFLAFLAFLAFLAFLA 160
Db 61 DMSRLKRRYLHSSQFLDLAVLSQPLTDLVLSDFPKTPVVRINKFLSPLSALEMETR 120
QY 161 TAYNPAFRIAKMLYFVVIHNSCLYFALSRYLGFGRDAWVYPPAOPGFRRLROYLY 220
Db 121 TAYNPIRISKMLILFILHMAACLYFALSRYLGFGRDAWVYPPAOPGFRRLROYLY 220
QY 221 SFVFTLITLTVDTPPPAAREERYLFMVGDPLLAWVGFATMGSSVYVNTADAAY 280
Db 181 SFVFTLITLTVDTPPPAAREERYLFMVGDPLLAWVGFATMGSSVYVNTADAAY 280
QY 281 PDHALVKKYMKLQHVNRKLERVIMYQHLQINKKMTNEVALQHLPERLRAEVAVSYL 340
Db 241 PNHLEVRSLYLRSRINKALHNVTWYOHILINKKITRENEILOQLPVLQTAIVAVHL 300
QY 341 STLSRVQIFONCEASLLELVKLQOPVYSPGEVYCRKGDIGEMVYIIRSGQLAVVADG 400
Db 301 PLISKVITFONCESSLEELVILKLPVYNGEVYCRKGDVGHMYIIRKGLAVVADG 360
QY 401 ITQYAVLGAIFYGFIISINIKMNSGNRRRTANIKSLGYSDLFCLSKEDLREVLSPQA 460
Db 361 VTQFVAVLDGNFPGISLILNKMGKSGNRRRTANIRISIGSDLFCLSKEDLREVLSPQA 420
QY 461 OTIMEEKKREIILKNNKLDVNAEAALQEAATESRLRGIDQDLQTYFARLAELES 520
Db 421 KRLLEEKROILTKMGMEISDECE--EKEKLEDKKRLLESSLETLQTKLNLWELLES 478
QY 521 SALKIAYRIELEMOTEMPEPDL-----AAADDEGEPE-----EGTSKDEGRASQ 568
Db 479 SVROMGRVDELELQTDG---EGIVAEGAGSESDDETERKRDVGDGEBOGEEPOBERG 535
QY 569 EGPGGPE 575
Db 536 EGDOGEE 542

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RESULT 5  
Q8CFV6 PRELIMINARY; PRT; 631 AA.

AC 08CFV6; DT 01-MAR-2003 (Tremblrel. 23, Created)  
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)  
DE Cyclic nucleotide gated channel alpha 3.  
GN Name=Cnga3.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Eye;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stadelton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,  
RA Brownstein M.J., Udell T.B., Roshtki S., Carninci P., Prange C.,  
RA Raha S.S., Lomuelano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.U., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Villalón D.K., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huijck S.W.,  
RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Kiryushki M.I., Skalka U., Smilun D.E., Scherch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Eye;  
RA Strausberg R.;  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Eye;  
RA Strausberg R.;  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC035272; AAH35272.1; -;  
DR EMBL; BC049145; AAH49145.1; -;  
DR MGI; MGI:1341818; Cnga3.  
DR GO; GO:0005221; F:intracellular cyclic nucleotide activated c. .; IPT.  
DR InterPro; IPR000595; CNMP binding.  
DR InterPro; IPR003938; EAG ELK ERG.  
DR InterPro; IPR005821; Ion trans.  
DR Pfam; PF00027; CNMP binding; 1.  
DR InterPro; IPR01622; K-channel pore.  
DR Pfam; PF00520; Ion trans; 1.  
DR PRINTS; PR01463; EAGCHANLMLY.  
DR SMART; SM0100; CNMP; 1.  
DR PROSITE; PS00888; CNMP-BINDING\_1; 1.  
DR PROSITE; PS00889; CNMP-BINDING\_2; 1.  
DR PROSITE; PS00890; CNMP-BINDING\_3; 1.  
DR Ion transport; Ion channel; Transmembrane; Transport.  
SQ SEQUENCE 631 AA; 72701 MW; 4FAD6E63A8A3FE6C CRC64;

Query Match 52.9%; Score 1582.5; DB 2; Length 631;  
Best Local Similarity 54.6%; Pred. No. 1.4e-98;  
Matches 297; Conservative 108; Mismatches 128; Indels 11; Gaps 3;

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QY 2 SQDTKVTYKTESS-----PPAPSKARKLLP-VLDSDGYIYVNTMWFPMVNYLII 51
Db 67 SELKEVSTRESNAQNPQKPPDQGEGRKEEPIYVDSSNITYRWLTAALPVFYNMCL 126
QY 52 IVCRACFDLOHGIVLAVLVDTSDLLVLDVVRVFRHTGFEQGLIVVDKGRISRYR 111
Db 127 IVCRACFDLOHGIVLAVLVDTSDLLVLDVVRVFRHTGFEQGLIVVDKGRISRYR 111
QY 112 TWSFPLDLASLMPDVTDVYVRLGPHPTLRFLAFLAFLAFLAFLAFLAFLAFLA 171
Db 187 TLHFKLIDILSLIPDLAVILKLVGVVPELRNRLIKTSRLFEFDRTRTNVNVIRICN 246
QY 172 IMLYIFVVIHNSCLYFALSRYLGFGRDAWVYPPAOPGFRRLROYLYSPVFTLITLT 231
Db 247 LVLTITLIHNNACTYFALSRYLGFGRDAWVYPPAOPGFRRLROYLYSPVFTLITLT 231
QY 232 VGDTPPAREERYLFMVGDPLLAWVGFATMGSSVYVNTADAAYPPDHALVKKYK 291
Db 307 IGETPPVKKDEEYLFVVIDPLVIGILFATIVGVGSMISNNAAPVEFOAKIDSYQVWQ 366
QY 292 LOHNRKLERVIMYQHLQINKKMTNEVALQHLPERLRAEVAVSYLSTSRVQIFON 351
Db 367 FRKVTYKDLERVIMYQHLQINKKMTNEVALQHLPERLRAEVAVSYLSTSRVQIFON 351
QY 352 CEASLLEELVKLQOPVYSPGEVYCRKGDIGEMVYIIRSGQLAVVADGCIQYAVLAGL 411
Db 427 CEAGLLVLEVLKLPVYSPGEVYCRKGDIGEMVYIIRSGQLAVVADGCIQYAVLAGL 411
QY 412 YFEISIIINIKMNSGNRRRTANIKSLGYSDLFCLSKEDLREVLSEYPOAOTIMEEKE 471
Db 487 YFEISIIINIKMNSGNRRRTANIKSLGYSDLFCLSKEDLREVLSEYPOAOTIMEEKE 471
QY 472 LKNNKLDVNAEAALQEAATESRLRGIDQDLQTYFARLAELESALKIAYRIER 531

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ID	Q9QNM7	PRELIMINARY:	PRT:	611 AA.
AC	Q9QNM7			
DT	01-MAY-2000 (Tremblrel. 13, Created)			
DT	01-MAY-2000 (Tremblrel. 13, Last sequence update)			
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)			
DE	Cyclic nucleotide-gated channel.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
DR	InterPro: IPR000595; cNMP binding.			
DR	InterPro: IPR005821; Ion Chan.			
DR	InterPro: IPR001622; K+-channel_pore.			
DR	Pfam; PF00027; cNMP_binding_1.			
DR	Pfam; PF00520; Ion_trans_1.			
DR	PROSITE; PS00868; cNMP_BINDING_1; 1.			
DR	PROSITE; PS00869; cNMP_BINDING_2; 1.			
DR	PROSITE; PS00042; cNMP_BINDING_3; 1.			
KW	cNMP-binding; Ion transport; Ionic channel; Multigene family;			
FT	TRANSMEM 186 206 Potential.			
FT	TRANSMEM 322 342 Potential.			
FT	TRANSMEM 398 418 Potential.			
FT	NP_BIND 501 624 cNMP.			
FT	BINDING 568 568 cNMP (Potential).			
FT	BINDING 583 583 cNMP (Potential).			
SO	SEQUENCE 706 AA; 81132 MW; F49900CD29B56239 CRC64;			
Query Match	52.8%; Score 1579; DB 1; Length 706;			
Best Local Similarity	52.7%; Pred. No. 2,9e-98;			
Matches 297; Conservative 111; Mismatches 138; Indels 18; Gaps 3				
QY	3	ODTKYKTTESAP-----PAPSKARKLLPLVDPGSDYDYYMLNTMVEPMVNLILVCR	55	
DB	149	KDRAKKEKKEKKEKKEKKEKPKKEEKCKGSVMDEPSNNYTHMLYIAVAVFNNCLLVR	208	
QY	56	ACFPDLQHGVLVAMLVLDYTSDLLVLDVYRFHTGFLTEGCLLVVDKGRISRRYRTWSF	115	
DB	209	ACFDELQEHMLMLVLDYDSADILYGMNMLVRARGTGLEQGLMVDASRLMGHYQTTHF	268	
QY	116	FLDLASLPTDQVYVYRGLGPHPTLRNLNFLAARLFEAFDRERTETAYANARIKLMY	175	
DB	269	KLDVLSLPTDLAFLYKGMNPELRFNRLKLARLFEFFDRTRRTYNNMFRIGNLVLY	328	
QY	176	IFVVYHNMSCLYPLSRILYFGGRDAWVYPPDAPQGFERLRQLYLXFSEFTLILTTVGT	235	
DB	329	ILIIIIHMACLYFAISKEITGFQTSWVPVNSNPFYGRLSKRYISLYWSTLTITIGET	388	
QY	236	PPPAEEBYLPMVGDFLVAVGWGAFATIMSGMSVYNNMTADAAFYPDHALVKKMKLQHV	295	
DB	389	PPPKVDEBYLVLVIDFLVGLVILPATVGVSGMISNNASRAEFQAKIDISIKQYQFRKY	448	
QY	296	NRLKERRVYDYOHLQIKKKMTNEVALIOHLPERLRAEVASVHLSTLSRVQIFQNCES	355	
DB	449	TKDLSTRYIRMFYDMANKKTVDEKEVKSJLPDKAKAETAIIVHDLTLRKVRIPODCBG	508	
QY	356	LLEELVYLQOQYTSRGSEYVCRKGIQGOBMTYIREGOLAVVADGDTTOYAVGAGLPG	415	
DB	509	LLELVYLRLRAVVSPEGDYICKKGIGREMYIKSGKLAVAADGTLQVVLADGSGFEE	568	
QY	416	ISIIINIKMGSGNRTANIKSLGYSDLCLSKEDREVLSEYPOAQTTMEKGRILLNK	475	
DB	569	ISIIINIKSGSKGNRTANIRISIGYDDLCLSDMDLMEALTEVPEAKKMLEEKGROILMD	628	
QY	476	NKLD----VNAEAELAQETSRRLGLDQDLDTQTFARLLAELESSALKIAYRIE	530	
DB	629	NLIIDELAKAGADPRDI-----EEKVHELTSTLSDLSQTRFARLLAEVATQMKVQORLS	682	
QY	531	RLEWQTRMPMPEDLAADDEGEP	554	
DB	683	QLSEGVKMLPPDGDAPQTEASQP	706	
RESULT 7				
Q9QNM7				
AC	Q9QNM7			
DT	01-MAY-2000 (Tremblrel. 13, Created)			
DT	01-MAY-2000 (Tremblrel. 13, Last sequence update)			
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)			
DE	Cyclic nucleotide-gated channel.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_Taxid=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 EX MEDLINE=97426406; PubMed=9278419;  
 RA Miaka T., Kusakabe Y., Emori Y., Gonoi T., Arai S., Abe K.;  
 RT "Taste buds have a cyclic nucleotide-activated channel, CNVGust.";  
 RL J. Biol. Chem. 272:22623-22629(1997).  
 DR EMBL; AB002801; BAA24353.1; -.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005216; F:ion channel activity; IEA.  
 DR GO; GO:0005267; F:potassium channel activity; IEA.  
 DR GO; GO:0006811; P:ion transport; IEA.  
 DR GO; GO:0006813; P:potassium ion transport; IEA.  
 DR InterPro; IPR000595; cAMP binding.  
 DR InterPro; IPR005821; Ion trans.  
 DR InterPro; IPR001622; K-channel pore.  
 DR Pfam; PF00027; cAMP\_binding; 1.  
 DR Pfam; PF00520; Ion\_trans; 1.  
 DR SMART; SMO0100; cAMP; 1.  
 DR PROSITE; PS00888; cAMP\_BINDING\_1; 1.  
 DR PROSITE; PS00889; cAMP\_BINDING\_2; 1.  
 DR PROSITE; PS00442; cAMP\_BINDING\_3; 1.  
 KW Ion transport; Ionic channel; Transmembrane; Transport.  
 SQ SEQUENCE 611 AA; 70399 MW; 9ACECEP9EEF63AC4 CRC64;

Query Match 52.8%; Score 1578; DB 2; Length 611;  
 Best Local Similarity 54.5%; Pred. No. 2.7e-98;  
 Matches 300; Conservative 105; Mismatches 125; Indels 20; Gaps 5;

OY 14 PPAPSKARKLKP-VLDPSGDYVYVWMLNTVPVWYNTLIIVCRACFPDLOHGYVAVMLVL 72  
 DB 68 PPEGKGRKKKPIVVDPSNNIYYRWLTAIPVFNWCLVCRACFDELOSHLTWMLVL 127  
 OY 73 DYTSDLVLLDMVYVFRHTGLEOGILVVDKGRISRRYRTVSFFLDASLMPDTPVYVRL 132  
 DB 128 DYSALALVVDMLVARVARGFLEOGIMVDRTKRLMGRHYTKTLHPKLDLSLPTDLAVLYKL 187  
 OY 133 GPHPTLRLNPLRLAPRLFEAPDRTERTAAPNAFRILKMLYIFVVIHNSCLYFALSRL 192  
 DB 188 GNNYPELRFNRLRLRSRLFEFFDRTERTNYPNFRIGNLVLYTLIIHMAACIFYALSK 247  
 OY 193 YLFGSRDAMVYPDPAQGFEBRLROYLYSFYSTLILTTVGDTPPAREEYLFVWGDPL 252  
 DB 248 FIGGTDSWVYVNPNSKPEYGRLSRKYISLYWSTLTLTIGETPPPVXDDEYLFVVIDFL 307  
 OY 253 LAVMGFATIMSGSVIYNNMTADAFYPDHALVKKYMKLOHVNKLERRYVDWYQHLQI 312  
 DB 308 VGVLIFFATIVGVSGSMISNNASRAEFOAKIDSIKQYQFRKVTYKDLSTRVIRWFDYIWA 367  
 OY 313 NKMTNEVALIOLHPERLRAEVAVSVHLSTLSRVOIFONCEASLLEELVTLKLOPOTSPG 372  
 DB 368 NRKTVDEKVEVLKNLPDKLKAELAINVHLDLTKKVRIFQDCBAGLVELVTLKRPVAFSPG 427  
 OY 373 EYVCRKGIQGEYMTIIRRGQLAVVADGIGTQYAVLGAGLYGEGISIIINIKSGNSGRRTA 432  
 DB 428 DYICKKGIGREMYTIKRGKLAIVADGVTQFVVLSDSYFGEISIIINIKSGNSGRRTA 487  
 OY 433 NIKSLGYSDLPCLSKEDLREVLSEYPOAQTIIEEKGREILIKMKNDL-----VNAEALEI 487  
 DB 488 NIKSLGYSDLPCLSKEDLREVLSEYPOAQTIIEEKGREILIKMKNDLIDDDLVTAADARNI 547  
 OY 488 ALOEATERSRLNGLDLQOTKFAALLAELESSAKIAYRIERLEWQ-TR-----EW 539  
 DB 548 -----EKVEYLESSLDGLQTRFARLLAEVYASQMKLKORLSQLESQWTRRGHGFSDR 601  
 OY 540 EMPEDLAED 549  
 DB 602 ENSEBASKAD 611

RESULT 8  
 Q9ER32

ID Q9ER32 PRELIMINARY; PRT; 632 AA.  
 AC Q9ER32;  
 DT 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
 DE Cyclic nucleotide-gated channel 2a.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_Taxid=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Olfactory epithelium, and Retina;  
 RA MEDLINE=20442421; PubMed=10984544;  
 RX Meyer M.R., Angele A., Kremer B., Kaupp U.B., Mueller F.;  
 RT "A cGMP-signalling pathway in a subset of olfactory sensory neurons";  
 RL Proc. Natl. Acad. Sci. U.S.A. 97:10595-10600(2000).  
 DR EMBL; AJ272429; CAC09431.1; -.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005216; F:ion channel activity; IEA.  
 DR GO; GO:0005267; F:potassium channel activity; IEA.  
 DR GO; GO:0006811; P:ion transport; IEA.  
 DR GO; GO:0006813; P:potassium ion transport; IEA.  
 DR InterPro; IPR000595; cAMP binding.  
 DR InterPro; IPR005821; Ion trans.  
 DR InterPro; IPR001622; K-channel pore.  
 DR Pfam; PF00027; cAMP\_binding; 1.  
 DR Pfam; PF00520; Ion\_trans; 1.  
 DR SMART; SMO0100; cAMP; 1.  
 DR PROSITE; PS00888; cAMP\_BINDING\_1; 1.  
 DR PROSITE; PS00889; cAMP\_BINDING\_2; 1.  
 DR PROSITE; PS00442; cAMP\_BINDING\_3; 1.  
 KW Ion transport; Ionic channel; Transmembrane; Transport.  
 SQ SEQUENCE 632 AA; 72535 MW; 248BAECCDD600D37 CRC64;

Query Match 52.8%; Score 1578; DB 2; Length 632;  
 Best Local Similarity 54.5%; Pred. No. 2.9e-98;  
 Matches 300; Conservative 105; Mismatches 125; Indels 20; Gaps 5;

OY 14 PPAPSKARKLKP-VLDPSGDYVYVWMLNTVPVWYNTLIIVCRACFPDLOHGYVAVMLVL 72  
 DB 89 PPEGKGRKKKPIVVDPSNNIYYRWLTAIPVFNWCLVCRACFDELOSHLTWMLVL 148  
 OY 73 DYTSDLVLLDMVYVFRHTGLEOGILVVDKGRISRRYRTVSFFLDASLMPDTPVYVRL 132  
 DB 149 DYSALALVVDMLVARVARGFLEOGIMVDRTKRLMGRHYTKTLHPKLDLSLPTDLAVLYKL 208  
 OY 133 GPHPTLRLNPLRLAPRLFEAPDRTERTAAPNAFRILKMLYIFVVIHNSCLYFALSRL 192  
 DB 209 GNNYPELRFNRLRLRSRLFEFFDRTERTNYPNFRIGNLVLYTLIIHMAACIFYALSK 268  
 OY 193 YLFGSRDAMVYPDPAQGFEBRLROYLYSFYSTLILTTVGDTPPAREEYLFVWGDPL 252  
 DB 269 FIGGTDSWVYVNPNSKPEYGRLSRKYISLYWSTLTLTIGETPPPVXDDEYLFVVIDFL 328  
 OY 253 LAVMGFATIMSGSVIYNNMTADAFYPDHALVKKYMKLOHVNKLERRYVDWYQHLQI 312  
 DB 329 VGVLIFFATIVGVSGSMISNNASRAEFOAKIDSIKQYQFRKVTYKDLSTRVIRWFDYIWA 388  
 OY 313 NKMTNEVALIOLHPERLRAEVAVSVHLSTLSRVOIFONCEASLLEELVTLKLOPOTSPG 372  
 DB 389 NRKTVDEKVEVLKNLPDKLKAELAINVHLDLTKKVRIFQDCBAGLVELVTLKRPVAFSPG 448  
 OY 373 EYVCRKGIQGEYMTIIRRGQLAVVADGIGTQYAVLGAGLYGEGISIIINIKSGNSGRRTA 432  
 DB 449 DYICKKGIGREMYTIKRGKLAIVADGVTQFVVLSDSYFGEISIIINIKSGNSGRRTA 508  
 OY 433 NIKSLGYSDLPCLSKEDLREVLSEYPOAQTIIEEKGREILIKMKNDL-----VNAEALEI 487  
 DB 509 NIKSLGYSDLPCLSKEDLREVLSEYPOAQTIIEEKGREILIKMKNDLIDDDLVTAADARNI 568  
 OY 488 ALOEATERSRLNGLDLQOTKFAALLAELESSAKIAYRIERLEWQ-TR-----EW 539

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Db 569 -----EKEVEYLESSLDGLQTRFARLLAEVSASQMKLKORLSQLESQWTRRGHGFSPDR 622
Qy 540 PMPEDLAEND 549
Db 623 ENSEDAKAD 632

RESULT 9
Q9ER33 PRELIMINARY; PRT; 670 AA.
ID Q9ER33;
AC Q9ER33;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Cyclic nucleotide-gated channel 2b.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=olfactory epithelium;
RC MEDLINE=20442421; PubMed=10984544;
RA Meyer M.R., Angele A., Krenner E., Kaupp U.B., Mueller F.;
RT "A cGMP-signalling pathway in a subset of olfactory sensory neurons.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:10595-10600(2000).
DR EMBL, AJ272428; CAC09430.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005216; P:ion channel activity; IEA.
DR GO; GO:0005267; P:potassium channel activity; IEA.
DR GO; GO:006811; P:ion transport; IEA.
DR GO; GO:006813; P:potassium ion transport; IEA.
DR InterPro; IPR000595; CNMP_binding.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR001622; K+channel_pore.
DR Pfam; PF00027; CNMP_binding.1.
DR Pfam; PF00520; Ion_trans.1.
DR SMART; SM00100; CNMP.1.
DR PROSITE; PS00888; CNMP_BINDING_1; 1.
DR PROSITE; PS00889; CNMP_BINDING_2; 1.
DR PROSITE; PS50042; CNMP_BINDING_3; 1.
DR Ion_transport; Ion channel; Transmembrane; Transport.
KW ION CHANNEL; IONIC CHANNEL; TRANSMEMBRANE; TRANSPORT.
SQ SEQUENCE 670 AA; 76420 MW; 65203ADE6F85F62 CRC64;

Query Match 52.8%; Score 1578; DB 2; Length 670;
Best Local Similarity 54.5%; Pred. No. 3, 1e-98;
Matches 300; Conservative 105; Mismatches 125; Indels 20; Gaps 5;

Qy 14 PAPSKARLRLP-VLDPSGDYVYWMINTVFPVMVNLILVGRACPPDLQHGVLAVLV 72
Db 127 PEGGKGRKQDPIVVDPSNITRYRLITAIALFVFNWCLLVGRACDELQSEHLTMTLV 186
Qy 73 DYTSLLLVLDNVVRFHGTLEQGLLVNDKGRISRRYVTSWFFLDLASEPTDVVYVL 132
Db 187 DYSADALVYVDMVLRARGTLEQGLVAVRDTKRLMKRYTTLHPKDIILSLIPDLAVYKL 246
Qy 133 GHTPTLRLARFLRLARFLRFLRFLRFLRFLRFLRFLRFLRFLRFLRFLRFLRFLR 192
Db 247 GMYVDELRLRNLRLRSLRFLRFLRFLRFLRFLRFLRFLRFLRFLRFLRFLRFLR 306
Qy 193 YLGFPRDAVYVDDPQGFRLRROVLYSFYSTLTITVGPDPARREELVEMGDPL 252
Db 307 FLGFGTDSVNVYVNTSFEYGRSLRKTIYLYWSTLTITIGTFPPVQDEELFVVIDPL 366
Qy 253 LAVMGFATTGSMSSVYVNMNTADAAYPDHALVKKYMKLQVNRRLERRVLDWYQHL 312
Db 367 VGVLLFATIVGVNVSWMNNSRAEFQAKIDSIKQYMFRTKTKLFRVIRWFDYLA 426
Qy 313 NKKMTNEVALIQHLPRLRLAEVAVSVHSLTSVVOIFQNCESLSEELVTLKIQPQYVSG 372
Db 427 NKRVTDEKSVLNPDLKLAELIAINVHLDLTKKVRIFQDCGGLVLELVLRPAVFSFG 486
Qy 373 EYVCRKGDIGEMVYIIRREGQLVAVDADGITQYAVLGAGLYFGBISITINIKGNSGNRRPA 432

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Db 487 DYICKGDIIGEMVYIIRREGQLVAVDADGITQYAVLGAGLYFGBISITINIKGNSGNRRPA 546
Qy 433 NIKSLGYDPLCLSEDLREVLSFYPQQTMEEGREILKMTLD-----VNAEAEI 487
Db 547 NIRSIGYDPLCLSEDLREVLSFYPQQTMEEGREILKMTLD-----VNAEAEI 606
Qy 488 ALQEATESRLKGLDQDLQTFARLLAEVSALKAIVRIERLEWO-TR-----EW 539
Db 607 -----EKEVEYLESSLDGLQTRFARLLAEVSASQMKLKORLSQLESQWTRRGHGFSPDR 660
Qy 540 PMPEDLAEND 549
Db 661 ENSEDAKAD 670

RESULT 10
CNG3_MOUSE
ID CNG3_MOUSE STANDARD; PRT; 631 AA.
AC 09JZ8; Q9WV01;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cyclic-nucleotide-gated cation channel alpha 3 (CNG channel alpha 3)
DE (CNG-3) (CNG3) (Cyclic nucleotide-gated channel alpha 3) (Cone
DE photoreceptor cGMP-gated channel alpha subunit).
GN Name=Cng3; Synonyms=Cng3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Retina;
RC MEDLINE=20273944; PubMed=10813773;
RX DOI=10.1002/(SICI)1096-9861(20000522)421:1<80::AID-CNE5>3.0.CO;2-O;
RA Hirano A.A., Hack I., Messle H., Duvolski R.M.;
RT "Cloning and immunocytochemical localization of a cyclic nucleotide-
RT gated channel alpha-subunit to all cone photoreceptors in the mouse
RT retina.";
RL J. Comp. Neurol. 421:80-94(2000).
RN [2]
RP SEQUENCE OF 95-631 FROM N.A.
RC STRAIN=129/Sv;
RX MEDLINE=99307448; PubMed=10377453;
RA Biel M., Seeliger M., Pfeiffer A., Kohler K., Gerschner A., Ludwig A.,
RA Jaisle G., Fauser S., Zrenner E., Hofmann F.;
RT "Selective loss of cone function in mice lacking the cyclic
RT nucleotide-gated channel CNG3.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:7553-7557(1999).
RN [3]
RP FUNCTION, AND SUBUNIT.
RX MEDLINE=20130348; PubMed=10662822;
RA Gerschner A., Zong X., Hofmann F., Biel M.;
RT "Molecular cloning and functional characterization of a new modulatory
RT cyclic nucleotide-gated channel subunit from mouse retina.";
RL J. Neurosci. 20:1324-1332(2000).
RN [4]
RP FUNCTION: Visual signal transduction is mediated by a G-protein
coupled cascade using cGMP as second messenger. This protein can
be activated by cyclic GMP which leads to an opening of the cation
channel and thereby causing a depolarization of cone
photoreceptors. Essential for the generation of light-evoked
electrical responses in the rod-, green- and blue sensitive cones
(Bay similarity). Induced a flickering channel gating, weakened the
outward rectification in the presence of extracellular calcium,
increased sensitivity for h-cis diltiazem and enhanced the cAMP
efficacy of the channel when coexpressed with CNGB3.
CC -1- SUBUNIT: Heterooligomeric complex with CNGB3.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Prominently expressed in retina.
CC -1- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
(CC 1.A.1.5) family.
CC -1- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.

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FT TRANSMEM 350 369 H5 (Potential).
FT DOMAIN 370 453 Extracellular (Potential).
FT TRANSMEM 454 474 H6 (Potential).
FT DOMAIN 475 663 Cytoplasmic (Potential).
FT NP_BIND 462 584 CAMP (By similarity).
FT BINDING 521 521 CAMP (By similarity).
FT BINDING 536 536 CAMP (By similarity).
FT CARBOHYD 379 379 N-linked (GlcNAc...) (Probable).
SQ SEQUENCE 663 AA; 76014 MW; A866DAF9203844EF CR64;

Query Match 52.5%; Score 1568; DB 1; Length 663;
Best Local Similarity 54.2%; Pred. No. 1.5e-97;
Matches 292; Conservative 108; Mismatches 133; Indels 6; Gaps 2;

QY 18 SKARLLEVLDPSSGYIYVMTWVPPVYVNIILVCRACFPDLDHGIVLVNLDYISD 77
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 124 TKKKEFLVLPDAGGMYRWLFLLALPVLYNCLVVARCFSDLKGYIYVLDYISD 183
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 78 LLYLDMVVRPFTGFLGQGLVVDKGRISRVRTWSPFLDASLMPDVVVRGPHTP 137
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 184 VVYIDLPRLRTGFLGQGLVVDKGRISRVRTWSPFLDASLMPDVVVRGPHTP 243
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 138 TLRLNRPRLPRLPFAFDRTERTRAYVPAFRIAKMLYIFVYIHNSCLYFALSRYLGF 197
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 244 EVRFRLHFAFMPEFDRTERTRAYVPAFRIAKMLYIFVYIHNSCLYFALSRYLGF 303
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 198 RDAWYPPDPAOGFERLRQYLYSYFSTLITVGDTPPPAREBYELFMVGDFLAVWG 257
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 304 VDTWYPPITDEYGLSREYLYCYWSTLTITIGETPPPKDEBYELVVIDFLGLVI 363
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 258 FATINGSMSVYNNNTADAAFYPHALVKKYMKLOHVNRKERRIVDYOHLQINKMT 317
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 364 FATYGNVGSMTSMNATAEFOAKIDAVKHYMQPRKYSKEBAKIRIFDVLMTNKSIV 423
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 318 NEVALIQHLPERLRAEVAVSHLSTLSRVQIFQNCESASLLELVLKQDQYSPGEYCR 377
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 424 DEREVLYKQNPALKRAEIAINVLSTLKKVRIPODCAGGLVLELVKLRQVSPGDYICR 483
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 378 KDDIQGEMVYIIEGQAVAVADGITOYAVLGLYFGEISINIKNMGSRRTANIKSL 437
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 484 KDDIKEMVYIIEGQAVAVADGITOYAVLGLYFGEISINIKNMGSRRTANIKSL 543
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 438 GYSDFECLSKEDREVLSYPOAQTIMBEKREIILKNKLLDVNAEA--ETALOETATS 495
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 544 GYSDFECLSKEDREVLSYPOAQTIMBEKREIILKNKLLDVNAEA--ETALOETATS 599
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 496 RLKGLDQOQLDQTKFARLAELESSALKIAYRIERLEWQTRBWPMPEDLAADGEP 554
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 600 KLEQLETNMDLTLYTRFARLAEVYGAQOKLQKRIIVLETKMKQNNEDSLSDGMSNPP 658
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 12
CNG1_CHICK STANDARD; PRT; 735 AA.
AC 090805;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 29-MAR-2004 (Rel. 43, Last annotation update)
DE Cyclic nucleotide-gated channel, cone photoreceptor, alpha subunit
DE (CNG channel 1) (CNG-1).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBT_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93264082; PubMed=7684234;
RA Boettig W., Altenhofen W., Mueller F., Dose A., Illing M.,
RT "Rod and cone photoreceptor cells express distinct genes for cGMP-
RT gated channels."
RL Neuron 10:865-877(1993).

```

```

CC -! FUNCTION: Visual signal transduction is mediated by a G-protein
CC coupled cascade using cGMP as second messenger. This protein can
CC be activated by cyclic GMP which leads to an opening of the cation
CC channel and thereby causing a depolarization of cone
CC photoreceptors.
CC -! SUBCELLULAR LOCATION: Integral membrane protein.
CC -! SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
CC (TC 1.A.1.5) family.
CC -! SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL, X89598; CAA61757.1; -.
CC PIR, I50630; -.
CC InterPro, IPR000595; CNMP_binding.
CC InterPro, IPR005821; Ion_trans.
CC InterPro, IPR001622; K-channel_pore.
CC Pfam, PF00027; CNMP_binding; 1.
CC Pfam, PF00520; Ion_trans; 1.
CC PROSITE, PS00888; CNMP_BINDING_1; 1.
CC PROSITE, PS00889; CNMP_BINDING_2; 1.
CC PROSITE, PS50042; CNMP_BINDING_3; 1.
CC CAMP-binding; Ion transport; Ionic channel; Multigene family;
CC Transmembrane; Vslon.
CC FT DOMAIN 1 210 Cytoplasmic (Potential).
CC FT DOMAIN 211 230 H1 (Potential).
CC FT DOMAIN 231 243 Extracellular (Potential).
CC FT TRANSMEM 244 262 H2 (Potential).
CC FT TRANSMEM 263 286 Cytoplasmic (Potential).
CC FT TRANSMEM 287 306 H3 (Potential).
CC FT DOMAIN 307 344 Extracellular (Potential).
CC FT TRANSMEM 345 367 H4 (Potential).
CC FT TRANSMEM 368 419 Cytoplasmic (Potential).
CC FT TRANSMEM 420 439 H5 (Potential).
CC FT TRANSMEM 440 523 Extracellular (Potential).
CC FT TRANSMEM 524 544 H6 (Potential).
CC FT TRANSMEM 545 735 Cytoplasmic (Potential).
CC FT NP_BIND 532 654 CAMP (By similarity).
CC FT BINDING 591 591 CAMP (Potential).
CC FT BINDING 606 606 CAMP (Potential).
CC FT CARBOHYD 449 449 N-linked (GlcNAc...) (Potential).
CC FT SEQUENCE 735 AA; 85031 MW; A67ADPD942CEFC CR64;

Query Match 52.3%; Score 1562.5; DB 1; Length 735;
Best Local Similarity 53.5%; Pred. No. 3.9e-97;
Matches 299; Conservative 108; Mismatches 149; Indels 3; Gaps 3;

QY 3 QDTKVTSSPPAPSKARKLPLVDPGSDYVYVMTWVPPVYVNIILVCRACFPDQ 62
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 180 KDDK-KDDKDDKDDKDDKDDKDDKDDKDDKDDKDDKDDKDDKDDKDDKDDK 238
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 63 HGYLVAMVLDYTSLLVLDNVVRFHGFLEQGLVVDKGRISRYRTWSPFLDIASL 122
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 239 IDHILKMLFLDYCSIIYVDFMFFVRFRTGFLGQGLVVDKGRISRYRTWSPFLDIASL 298
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 123 MPTDVVVRPFTGFLGQGLVVDKGRISRVRTWSPFLDASLMPDVVVRGPHTP 182
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 299 LPTDLAVLKLGLNLYELRNRLRLARLPEAFDRTERTRAYVPAFRIAKMLYIFVYIH 358
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 183 NSCLYFALSRYLGFGRDAWVYPPDPAOGFERLRQYLYSYFSTLITVGDTPPPAREE 242
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 359 NACIFPALSRYLGFGRDAWVYPPDPAOGFERLRQYLYSYFSTLITVGDTPPPAREE 418
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 243 EYLFVAVGDFLLAVMGFATIMGSMVYNNNTADAAFYPHALVKKYMKLOHVNRKERR 302
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 419 EYLFVAVGDFLLAVMGFATIMGSMVYNNNTADAAFYPHALVKKYMKLOHVNRKERR 478
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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QY 303 VIDWYQHLOINKNKTEVAIIQHLPERLRRAVAVSHLSTLSRVOIFONCEASLJEVL 362  
 Db 479 VIKWFDYIMTKKTVDEKEVKNLPDKLKAELAINVHLDTLKKRIRIODEAGLITLVL 538  
 QY 363 KLOPQTSRPGYVYRKDIDIGEMYIIRREGOLAVVADGITOYAVLGLYFGEISITINIK 422  
 Db 539 KUKRTVSPDQYICKGIDIGEMYIIRREGOLAVVADGITOYAVLGLYFGEISITINIK 598  
 QY 423 GNNSGNRRNTANIKSLGYSDLFCLSKEDLREVLSEYPOAQITMEKREILLKNNKLDVNA 482  
 Db 599 GSKSGNRRNTANIRISGYSDLFCLSKEDLREVLSEYPOAQITMEKREILLKNNKLDVNA 658  
 QY 483 EAEIALQGEATRESLRGLDQDDLDQTKFARLAELESSALKTAVRIERLEWOTREMPMP 542  
 Db 659 AKAG-ADPKLEEKIDLELTDLTOTRFARLAEVSSSOQVKORLARIVETRVKKY-G 716  
 QY 543 EDLAEADDEGEPEEGTSKD 561  
 Db 717 GSLVGEPEPEKEPEQK 735

## RESULT 13

CNG2\_RABIT STANDARD; PRT; 664 AA.

AC Q28718;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Cyclic-nucleotide-gated olfactory channel (Cyclic-nucleotide-gated cation channel 2) (CNG-2) (CNG2) (Aorta CNG channel) (RACNG).  
 DE Name=CNG2; Synonyms=CNG2;  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Aorta;  
 RX MEDLINE=93359035; PubMed=7689061;  
 RA Biele M., Altenhofen W., Hüllin R., Ludwig J., Freichel M., Plocher V., Dascal N., Kaupp U.B., Hofmann F.;  
 RT "Primary structure and functional expression of a cyclic nucleotide-gated channel from rabbit aorta";  
 RL FEBS Lett. 329:134-138 (1993).  
 CC -1- FUNCTION: Odorant signal transduction is probably mediated by a G-protein coupled cascade using cAMP as second messenger. The olfactory channel can be shown to be activated by cyclic nucleotides which leads to a depolarization of olfactory sensory neurons.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel (TC 1.A.1.5) family.  
 CC -1- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.ebi.ac.uk/announcements> or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
 CC -----  
 CC EMBL: X59668; CAA42201.1; ALT INIT.  
 CC InterPro: IPR000595; cAMP binding.  
 CC InterPro: IPR005821; Ion Trans.  
 CC InterPro: IPR001622; K-channel\_pore.  
 CC Pfam: PF000027; cAMP\_binding; 1.  
 CC Pfam: PF005520; Ion\_trans; 1.  
 CC PROSITE: PS00888; cAMP\_BINDING\_1; 1.  
 CC PROSITE: PS00889; cAMP\_BINDING\_2; 1.  
 CC PROSITE: PS50042; cAMP\_BINDING\_3; 1.  
 CC Name=CNG2; Synonyms=Cng2;  
 CC cAMP-binding; Ion transport; Ionic channel; Multigene family;

KM Olfaction; Transmembrane.  
 FT DOMAIN 1 140  
 FT TRANSMEM 141 160  
 FT DOMAIN 161 173  
 FT TRANSMEM 174 192  
 FT DOMAIN 193 216  
 FT TRANSMEM 217 236  
 FT DOMAIN 237 274  
 FT TRANSMEM 275 297  
 FT DOMAIN 298 349  
 FT TRANSMEM 350 369  
 FT DOMAIN 370 453  
 FT TRANSMEM 454 474  
 FT DOMAIN 475 664  
 FT NP\_BIND 462 584  
 FT BINDING 521 521  
 FT BINDING 536 536  
 FT CARBOHYD 379 379  
 SQ SEQUENCE 664 AA; 76205 MW; 5E9170DB322B3E9 CRC64; (Potential).

Query Match 52.3%; Score 1562; DB 1; Length 664;  
 Beet Local Similarity 54.2%; Pred. No. 3.7e-97;  
 Matches 292; Conservative 108; Mismatches 133; Indels 6; Gaps 2;

QY 18 SKARKLLPVLDPSGDYVYVWMLNTWVFPVYVNLIIIVGRACFPDLOHGYVAVMLVDTSD 77  
 Db 124 TKKKFELFVLDPADMDYRMLFVIYANFVLNWCILVARACFSDLOQGYFLWMLVLDYFSD 183  
 QY 78 LLYLLDVAVRPHHTGELQGLIVVDKGRISRRYVTSFFPLDASLMPDTPVYVRLGPHTP 137  
 Db 184 VVYIADFLIRLRIGFLEQGLVVDKPKLRDNYIHTIQFLDVASIIPTDILYAVAGVHNP 243  
 QY 138 TLIRNRLRARPRLPEAFDRTEETRTAVPNARLAKMLTYVVIHNSCLFYALSRYLGRG 197  
 Db 244 ELRNRLLHARMEFFDRTEETRTSYNFIIRSNLVLYIVIHMAACIYVAISKISGFG 303  
 QY 198 RDAAVYVDPAPQPFERLRROYLYSFYSTLIITLVGDTPPAREEYLPFVVGDFLAWNG 257  
 Db 304 VDTWVYVNIITDPEYGLAREYICLYWSTLTLTITETPPVDEEYLVVIFDLGLVI 363  
 QY 258 FATITMSMSVYIYNNNTADAPFDHALYKTYKLOHVRKLERRYIDWYQHLOINKNKMT 317  
 Db 364 FATIVAVGSMISNMNATRAEFQAKIDAVYHVOQFKAKEAKVIKWFYIMTKKTV 423  
 QY 318 NEVAIIQHLPERLRRAVAVSHLSTLSRVOIFONCEASLJEVLVYKLOQOTSPPGYVYR 377  
 Db 424 DEREVAKNLPKARARAIANVHSLTKVRIIODEAGLITLVLKRPQVSPDQYICR 483  
 QY 378 KGDIGEMYIIRREGOLAVVADGITOYAVLGLYFGEISITINIKGNNSGNRRNTANIKSL 437  
 Db 484 KGDIGEMYIIRREGOLAVVADGITOYAVLGLYFGEISITINIKGNNSGNRRNTANIRSL 543  
 QY 438 GYSDLFCLSKEDLREVLSEYPOAQITMEKREILLKNNKLDVNAEAA--EIALDEATES 495  
 Db 544 GYSDLFCLSKEDLREVLSEYPOAQITMEKREILLKNNKLDVNAEAA--EIALDEATES 599  
 QY 496 RLRGLDQDDLDQTKFARLAELESSALKTAVRIERLEWOTREMPMPDLAEADDEGP 554  
 Db 600 KIKOLETNNMETLYTRFGRILAEYTAQKIKRITVLEVKQNTEDYDLSGNNSPBP 658  
 RESULT 14  
 CNG2\_RAT STANDARD; PRT; 664 AA.  
 AC Q00195;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Cyclic-nucleotide-gated olfactory channel (Cyclic-nucleotide-gated cation channel 2) (CNG-2) (CNGC1).  
 DE Name=Cng2; Synonyms=Cng2;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;





DR EMBL; BC048775; AAH48775.1; -.  
 DR MGD; MGI:108040; Cnga2.  
 DR GO; GO:0005216; P:ion channel activity; IMP.  
 DR GO; GO:0007608; P:perception of smell; IMP.  
 DR InterPro; IPR000595; CNMP binding.  
 DR InterPro; IPR003938; EAG\_ELK\_ERG.  
 DR InterPro; IPR005821; Ion trans.  
 DR InterPro; IPR001622; K+channel pore.  
 DR Pfam; PF00027; CNMP binding; 1.  
 DR Pfam; PF00520; Ion trans; 1.  
 DR PRINTS; PR01463; EAGCHANLFWLY.  
 DR SMART; SM00100; CNMP\_1.  
 DR PROSITE; PS00888; CNMP\_BINDING\_1; 1.  
 DR PROSITE; PS00889; CNMP\_BINDING\_2; 1.  
 DR PROSITE; PS50042; CNMP\_BINDING\_3; 1.  
 DR Ion transport; Ionic channel; Transmembrane; Transport.  
 KW ION CHANNEL; ION CHANNEL; TRANSPORT;  
 SQ SEQUENCE 664 AA; 76192 MW; 34F8DF3B372C0D9C CRC64;

Query Match 52.1%; Score 1558; DB 2; Length 664;  
 Best Local Similarity 54.2%; Pred. No. 6; 9e-97;  
 Matches 292; Conservative 107; Mismatches 134; Indels 6; Gaps 2;

QY 18 SKARLLVLPDSSGDYYWMTWVPMVYNLIIVCRACFPDLOHGYIVAMLVLDYTS 77  
 Db 126 TKKKEFLVLDPAQDWMYRMLFVIAMPVLYNCLVAPACFSDDLQNYFVWLVLDYPSD 185  
 QY 78 LLYLDWVVRPHTGFLVLEQILVVDKGRISRYRTWSPFLDLASIMPTDVVYVRLGPHTP 137  
 Db 186 TVYINDLIIRLTGFLVLEQILVVDKGRISRYRTWSPFLDLASIMPTDVVYVRLGPHTP 245  
 QY 138 TLRLNRFAPRLFAFRTETRTAYPNAFRIAKMLLYIFVVIHNSCLYFALSRYLFG 197  
 Db 246 EVRFNRRLHFAFMFEPFRTETRTSYPMIFRISNLVLYLVIHNNACIYVAISKISGFG 305  
 QY 198 RDAWYPPDPAQGFRLRQVLYSFYFSLTLITVGDTPPPAREEYLFMVGDPELLAMG 257  
 Db 306 VDTWYFNTDPEYGLAREYIYCYWSTLTLITGETPPVKDEEYLFVLPDFLIGVLI 365  
 QY 258 FATWGSMSVLYNNNTADAAFYPDHALVKKYMKLQHVNRKLERVIDMYCHLQINKKMT 317  
 Db 366 FATIVGNVSMISNNNATRAEFQAKIDAVKHMGFRKVSXOMEAVIKMFDVLTWTKTV 425  
 QY 318 NEVALIQHLPERLRAEVAVSVHLSTLSRVQIFQNCESLLEELVLIQPTYSPEEYVCR 377  
 Db 426 DEREVLKNLPKALRAEIAINVHLSTLKKVRIFQDCEAGLVELVLIKRPQVFPSPDYICR 485  
 QY 378 KADIGQEWYIIRREGQLAVVADGDTQYAVLAGLYFGESIIINIKNMSGNRRRTANIKSL 437  
 Db 486 KGDICKEMYIIKEGGLAVVADGDTQYAVLAGLYFGESIIINIKNMSGNRRRTANIKSL 545  
 QY 438 GYSDFCLSKEDLREVLSEYFQAQTIMKEKREILLKNNKLDVNAEAA-EIALQEATES 495  
 Db 546 GYSDFCLSKEDLREVLSEYFQAQTIMKEKREILLKNNKLDVNAEAA-EIALQEATES 601  
 QY 496 RLRLGDDQDLQTFARLALBSSAKIYVIRLELWQTRWMPMPEDLABADDEGEP 554  
 Db 602 KLEQLETMWTLYTRFARLALBSSAKIYVIRLELWQTRWMPMPEDLABADDEGEP 660

Search completed: February 10, 2005, 03:42:45  
 Job time : 116 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 9, 2005, 23:11:20 ; Search time 27 Seconds  
(without alignments)  
2049.061 Million cell updates/sec

Title: US-09-927-267-1

Perfect score: 2989

Sequence: 1 MSQDTKVKTTESPPAPSKA.....EGTSKDEGRASQGPPE 575

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2811	94.0	575	159327	olfactory cyclic n
2	1579	52.8	706	A55251	cyclic nucleotide-
3	1568	52.5	663	S11521	CAMP-gated channel
4	1562.5	52.3	735	150630	alpha subunit of c
5	1562	52.3	732	S35691	cyclic nucleotide-
6	1558	52.1	664	S11517	cyclic nucleotide-
7	1544.5	51.7	690	S07103	CAMP-gated ion cha
8	1542	51.6	695	S74179	cyclic nucleotide-
9	1538.5	51.5	686	A44842	CAMP-gated ion cha
10	1532.5	51.3	691	JC6509	rod cyclic nucleot
11	1529	51.2	645	150680	alpha subunit of r
12	1526.5	51.1	690	A42161	CAMP-gated cation
13	1525.5	51.0	688	B42161	CAMP-gated cation
14	1436.5	48.1	682	JH0560	cyclic nucleotide-
15	1235	41.3	665	S52072	DmCNC protein - f
16	1121.5	37.5	722	S28292	hypothetical prote
17	858	28.7	261	178560	cyclic nucleotide-
18	847	28.3	261	178559	cyclic nucleotide-
19	788.5	26.4	800	T19627	hypothetical prote
20	738	24.7	673	T20936	hypothetical prote
21	716	24.0	909	S32538	CAMP-gated cation
22	647	21.6	644	T33125	hypothetical prote
23	642	21.5	611	T20935	hypothetical prote
24	511.5	17.1	191	S74158	CAMP-gated cation
25	491.5	16.4	189	S74159	CAMP-gated cation
26	470.5	15.7	767	T21969	hypothetical prote
27	387.5	13.0	962	T53197	potassium channel
28	382.5	12.8	1087	T31100	probable potassium
29	382.5	12.8	1284	T13168	probable potassium

30	377.5	12.6	1174	2	A40853	potassium channel
31	377	12.6	989	2	I48912	potassium channel
32	375	12.5	1159	2	T38465	probable potassium
33	370	12.4	1102	2	T17367	potassium channel
34	365	12.2	934	2	T42394	potassium channel
35	362.5	12.1	514	2	T19579	hypothetical prote
36	362	12.1	1017	2	T33354	probable potassium
37	339.5	11.4	828	2	T52046	potassium channel
38	310.5	10.4	662	2	T04461	potassium channel
39	307.5	10.3	807	2	T12177	potassium channel
40	300	10.0	688	2	S55349	potassium channel
41	295.5	9.9	716	2	T51354	cyclic nucleotide-
42	293	9.8	787	2	S68699	potassium channel
43	285.5	9.6	845	2	T07052	probable potassium
44	269.5	9.0	887	2	T03939	potassium channel
45	268.5	9.0	838	2	S23606	potassium channel

#### ALIGNMENTS

##### RESULT 1

I59327 Olfactory cyclic nucleotide gated cation channel - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #ext\_change 09-Jul-2004

C/Accession: I59327; I58165

R/Bradley, J.; Li, J.; Davidson, N.; Lester, H.A.; Zinn, K.

Proc. Natl. Acad. Sci. U.S.A. 91, 8890-8894, 1994

A/Title: Heteromeric olfactory cyclic nucleotide-gated channels: A new subunit that con

A/Reference number: I59327; MUID:94377458; PMID:7522325

A/Accession: I59327

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-575 <RES>

A/Cross-references: UNIPROT:Q64359; EMBL:U12623; NID:G538128; PID:AAA21464.1; PID:G538

R/Lieman, E.R.; Buck, L.B.

Neuron 13, 611-621, 1994

A/Title: A second subunit of the olfactory cyclic nucleotide-gated channel confers high

A/Reference number: I58165; MUID:95000663; PMID:7522482

A/Accession: I58165

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-575 <RES>

A/Cross-references: EMBL:U12425; NID:G548083; PID:AAA64748.1; PID:G548084

C/Suprafamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

F/348-472/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 94.0%; Score 2811; DB 2; Length 575;

Best Local Similarity 93.4%; Pred. No. 3e-187;

Matches 537; Conservative 16; Mismatches 22; Indels 0; Gaps 0;

QY	1	MSQDTKVKTTESPPAPSKALPVLPDPSGDYYTWLNTWTFPVWYNTLLVGRACFPD	60
DB	1	MSQDGKVKTTESPPAPSKARLPLVLPDPSGDYYTWLNTWTFPVWYNTLLVGRACFPD	60
QY	61	LQHGVLVAVLVLDYSDLLYLDMVRFHTGFLFEGGILLVVDKGRISRRVYRTWSFLDIA	120
DB	61	LQHSYLVAVFVLDYSDLLYLIDIGVRFHTGFLFEGGILLVVDKGRISRRVYRTWSFLDIA	120
QY	121	SLMPTDVVYVVRGPHPTLRNRLRPARLFEAFDRTETRTAYPNAFRILAKMLYIFVYI	180
DB	121	SLVPTDAVVOLOPHPTLRNRLRFLRFLFAFDRTETRTAYPNAFRILAKMLYIFVYI	180
QY	181	HNNSCLYFALSRYLGFGRDAMYPPDAQGFELRRQYLYSYFESFLILTTVGDTPPPAR	240
DB	181	HNNSCLYFALSRYLGFGRDAMYPPDAQGFELRRQYLYSYFESFLILTTVGDTPPPAR	240
QY	241	EEBYLFMVGDELAVVGFATINGSMSVYNNMTADAAPYPDALVKKYMKLOHNVKXLE	300
DB	241	EEBYLFMVGDELAVVGFATINGSMSVYNNMTADAAPYPDALVKKYMKLOHNVKXLE	300
QY	301	RRVIDWYOHLOINKKMTNEVALLOHLPERLRAEVAVSVHLSTLSRVOIFONCEASLLBEL	360









Db 556 AGNRRRTANIKSIGSDLPCLSKDMLMEALTEYPAKTMLEBKQKQILMKDGLDINIANA 615

QY 486 EIALQEAVERSLRGDDQDDIQTKFARLLAEISSALKIAYRIERLE 533

Db 616 GSDPKD-LEBKTRMEGSDVLDQTRFARILAEYBESMOCKLKORLTKE 662

## RESULT 11

150680  
alpha subunit of rod photoreceptor CNG-channel - chicken  
C/Species: Gallus gallus (chicken)  
C/Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
C/Accession: 150680  
R/Bonfigli W.; Altenhofen, W.; Muller, F.; Dose, A.; Illing, M.; Molday, R.S.; Kaupp, U.E.  
Neuron 10, 865-877, 1993  
A/Title: Rod and cone photoreceptor cells express distinct genes for cGMP-gated channels  
A/Reference number: 150630; MUID:93264082; PMID:7684234  
A/Accession: 150680  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-645 <NON>  
A/Cross-references: UNIPROT:Q90980, EMBL:X69599, NID:9908852, PIND:CAA61758.1, PID:99088  
C/Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-  
F/431-555/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 51.2%; Score 1529; DB 2; Length 645;  
Best Local Similarity 50.7%; Pred. No. 3.2e-98;  
Matches 285; Conservative 144; Mismatches 143; Indels 10; Gaps 5;

QY 6 KYKTTSEPPAPAKRLPLVLDPSGDYYWMLNTWVPMVNTLILVCRACFPDLQHG 65

Db 89 KHKNGKKKKGEKKKKDIFIDPAGNMYNMLFCITMPVMYMTWIMRACFDELQNDY 148

QY 66 LVAMVLVDYSDLLYLDMVVRPHGFLGGLIVVDKGRISRYRTWSFFDLASLMT 125

Db 149 LAVMFLVDVSDVLYIADMFVTRTGYLQGLLVKEEQKLEKKEKSSLDQFKDLFLSLIPT 208

QY 126 DVVYVRLCPHPPTLRFLNRLFAAPRLFEAPDRTETRTAYPNARLAKMLYIFVYIHNMC 185

Db 209 DLVYFLGLNYPRLRLNRLNRLVARMFEFQRTETRTNRYNRIPLSNLWYIVIIHNNC 268

QY 186 LYFALSRYLGFGRDAWVYPPDAOPGFERLRQYLYSFYSTLILITVGDTPPAREEYL 245

Db 269 VVYSISKALIGFADTWVYPTSHPEPARLRLKRYVYLSLWSTLTLTIGETPPVARDSEYV 328

QY 246 FMVGDLLAVMGATIMSGSSVYNNMTADAFFYDHALVKKYMKLQHNRLLEBRVD 305

Db 329 FVVVDLAVGVLFATIVGNVSMISNNAPARAEFOAKIDAIKOYMFRTNVSQMEKRYIK 388

QY 306 WYOHQIQNKMTNEVALIQHLPRLRAEVAVSVHLSTLSRVQIFONCEASLLEELVYLQ 365

Db 389 WFLYLTNKKAVDERELKYLPRKLRARLAINVHLELKKVRIFFADCEAGLVELVYLQ 448

QY 366 PQYSPGEYVCRKGIQGEYIIREGQLAVVADDTQYAVLAGLYGEISIIINIKGM 425

Db 449 PQYVSPGDYICRKGDIIGREMYIIKEGKLAVVADDTQYFVVLSDGSYFGESIIINIKGS 508

QY 426 SGNRRRTANIKSIGSDLPCLSKEDRLREVSEYPOAQITMEKREIILKNNKLDVNAEA 485

Db 509 AGNRRRTANIKSIGSDLPCLSKDMLMEALTEYPAKTMLEBKQKQILMKDGLDII--EVA 566

QY 486 EIALQ- EATESRLRGDDQDDIQTKFARLLAEISSALKIAYRIERLEWQTEWMPMP- 543

Db 567 NIGSDPKDLEBKAVAYMGSDRLQTKFARLLAEYDAQGLKKRLQIEKILK--PVMQ 624

QY 544 ---DLAADDEGEPEEGTSKDE 562

Db 625 EPLDFEADPPTD-KPGVTYKTE 645

RESULT 12  
A42161  
cGMP-gated cation channel, rod photoreceptor - human

C/Species: Homo sapiens (man)  
C/Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 09-Jul-2004  
C/Accession: A42161  
R/Pittler, S.J.; Lee, A.K.; Altherr, M.R.; Howard, T.A.; Seldin, M.F.; Hurwitz, R.L.; Wa  
J. Biol. Chem. 267, 6257-6262, 1992  
A/Title: Primary structure and chromosomal localization of human and mouse rod photore  
A/Reference number: A42161; MUID:92210603; PMID:1372902  
A/Accession: A42161  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-690 <PIT>  
A/Cross-references: UNIPROT:P29973, GB:M84741; NID:9180461; PIND:AAA52010.1; PID:9180462  
C/Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-  
F/479-603/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 51.1%; Score 1526.5; DB 2; Length 690;  
Best Local Similarity 53.8%; Pred. No. 5.2e-98;  
Matches 284; Conservative 112; Mismatches 131; Indels 1; Gaps 1;

QY 6 KYKTTSEPPAPAKRLPLVLDPSGDYYWMLNTWVPMVNTLILVCRACFPDLQHG 65

Db 137 KKKKEKSKDKKHHKKGVVVIDSGNYYNMLFCITMPVMYMTWIMRACFDELQSDY 196

QY 66 LVAMVLVDYSDLLYLDMVVRPHGFLGGLIVVDKGRISRYRTWSFFDLASLMT 125

Db 197 LEVWILVDYSDIYVLDIMFVTRTGYLQGLLVKEELKILNKYKSNLQFKDLVLSLIPT 256

QY 126 DVVYVRLCPHPPTLRFLNRLFAAPRLFEAPDRTETRTAYPNARLAKMLYIFVYIHNMC 185

Db 257 DLVYFLGLNYPRLRLNRLNRLVARMFEFQRTETRTNRYNRIPLSNLWYIVIIHNNC 316

QY 186 LYFALSRYLGFGRDAWVYPPDAOPGFERLRQYLYSFYSTLILITVGDTPPAREEYL 245

Db 317 VVYSISKALIGFADTWVYPTSHPEPARLRLKRYVYLSLWSTLTLTIGETPPVARDSEYV 376

QY 246 FMVGDLLAVMGATIMSGSSVYNNMTADAFFYDHALVKKYMKLQHNRLLEBRVD 305

Db 377 FVVVDLAVGVLFATIVGNVSMISNNAPARAEFOAKIDAIKOYMFRTNVSQMEKRYIK 436

QY 306 WYOHQIQNKMTNEVALIQHLPRLRAEVAVSVHLSTLSRVQIFONCEASLLEELVYLQ 365

Db 437 WFDYLTNKKAVDERELKYLPRKLRARLAINVHLELKKVRIFFADCEAGLVELVYLQ 496

QY 366 PQYSPGEYVCRKGIQGEYIIREGQLAVVADDTQYAVLAGLYGEISIIINIKGM 425

Db 497 PQYVSPGDYICRKGDIIGREMYIIKEGKLAVVADDTQYFVVLSDGSTGEISIIINIKGS 556

QY 426 SGNRRRTANIKSIGSDLPCLSKEDRLREVSEYPOAQITMEKREIILKNNKLDVNAEA 485

Db 557 AGNRRRTANIKSIGSDLPCLSKDMLMEALTEYPAKTMLEBKQKQILMKDGLDIIINIANA 616

QY 486 EIALQEAVERSLRGDDQDDIQTKFARLLAEISSALKIAYRIERLE 533

Db 617 GSDPKD-LEBKTRMEGSDVLDQTRFARILAEYBESMOCKLKORLTKE 663

## RESULT 13

B42161  
cGMP-gated cation channel, rod photoreceptor - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 16-Jul-1999  
C/Accession: B42161  
R/Pittler, S.J.; Lee, A.K.; Altherr, M.R.; Howard, T.A.; Seldin, M.F.; Hurwitz, R.L.; Wa  
J. Biol. Chem. 267, 6257-6262, 1992  
A/Title: Primary structure and chromosomal localization of human and mouse rod photore  
A/Reference number: A42161; MUID:92210603; PMID:1372902  
A/Accession: B42161  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-688 <PIT>  
A/Cross-references: GB:M84742  
A/Note: authors translated the codon TAT for residue 544 as Thr



C:Superfamily: cyclic nucleotide-gated channel; CAMP receptor protein cyclic nucleotide-  
C:Keywords: cGMP binding  
F:447-599/Domain: CAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 51.0%; Score 1525.5; DB 2; Length 688;  
Best Local Similarity 51.9%; Pred. No. 66-98;  
Matches 289; Conservative 116; Mismatches 137; Indels 15; Gaps 4;

```

QY 6 KKTTESSPAPSKARKLLPVLDPGDDYVWMLNTMVPFVWNLIIIVGRACFPDLOHXY 65
DB 133 KKKKEKTEKKEBEKEKEVAVVDPNDPFGRLARKYVSLVWSTLTLTITGTPPVLDSEYI 192
QY 66 LVAMVLVDYSDLLYLDMVVRFHGTGLEQGLIIVDKGRISRYVWTSGFFDLASLMP 125
DB 193 LEYMLIFDVSNVNVVLIADMFVATRTGYLEQGLIIVDKRMLEKYKANLPKLDIVSLVT 252
QY 126 DVVYVRLGPHPTTLRLNRLPRLPRLPRLPRLPRLPRLPRLPRLPRLPRLPRLPRL 185
DB 253 DLLYIKFGWNYPEIRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRL 312
QY 166 LVFALSRVYLGFRDAMVYDPAQPGFERLRQYLSFVFSTLITLVGDPPTPARREBYL 245
DB 313 VYVTSKALGSPNDVWVYDPAQPGFERLRQYLSFVFSTLITLVGDPPTPARREBYL 372
QY 246 FMVGDPELLAVMGFATIMSGMSVIVYNNMTADAFYPDHALVKKYMKLQHNKRLERRVD 305
DB 373 FVYVDFLIGVLLFATIVGVSGISMNNAARAEFGORVDAIKQYNNFRVNSDMERVIK 432
QY 306 WYQHLQINKMTNEVALIQHLPERLRAEVAHSVHLSLRVQIPONCEASLLEBYLKLQ 365
DB 423 WFDYMTNKKTVDEQEVLLKLPDLKRAEIAINVHDLTKKRIIPDCEAGLLVEVLKLQ 492
QY 366 POTVSGEVYVCKGDIQGMYYIRREGQLAVVADDTQYAVAGAGYRGEISIIINIKGM 425
DB 493 PQVYVPGDITCKRGDIQGMYYIRREGQLAVVADDTQYAVAGAGYRGEISIIINIKGM 552
QY 426 SGNRRNTANIKSLGSDLPCLSKEDLREVLSEYPOAQTIIEEKGREILLKMKLDVNA 481
DB 553 AGNRRNTANIKSLGSDLPCLSKEDLREVLSEYPOAQTIIEEKGREILLKMKLDVNA 612
QY 482 -AEAAEIALQEAATESRLGLDQDLDTQTFARLLAELESSALKIAYRIERLEWQ 540
DB 613 GSDPMDL-----EEVYTRMEGSDVLDLQTRFACILAEVSMOQKLRQLTKVEKFKL-P 664
QY 541 WEEDLAEDDE--GPE 555
DB 665 LIETEFSALEPGESE 681

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## RESULT 14

JH0560  
Cyclic nucleotide-gated channel - channel catfish  
C:Species: Ictalurus punctatus (channel catfish)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #ext\_change 09-Jul-2004  
C:Accession: JH0560  
R:Goulding, B.H.; Ngai, J.; Kramer, R.H.; Colicos, S.; Axel, R.; Siegelbaum, S.A.; Chase  
Neuron 8, 45-58, 1992  
A:Title: Molecular cloning and single-channel properties of the cyclic nucleotide-gated  
A:Reference number: JH0560; MUID:92110008; PMID:1370374  
A:Accession: JH0560  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-682 <CGU>  
A:Cross-references: UNIPROT:P55934; GB:M83111  
A:Experimental source: Olfactory epithelium  
C:Comment: This cyclic nucleotide-gated channel is activated equally well by both CAMP &  
C:Superfamily: cyclic nucleotide-gated channel; CAMP receptor protein cyclic nucleotide-  
C:Keywords: cAMP binding; cGMP binding; ion channel; ion transport; olfaction; transmem-  
F:137-157/Domain: transmembrane #status predicted <TS1>  
F:173-193/Domain: transmembrane #status predicted <TS2>  
F:217-236/Domain: transmembrane #status predicted <TS3>  
F:241-261/Domain: transmembrane #status predicted <TS4>  
F:277-297/Domain: transmembrane #status predicted <TS5>

F:319-337/Domain: transmembrane #status predicted <TS5>  
F:350-370/Domain: transmembrane #status predicted <TS6>  
F:447-571/Domain: CAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 48.1%; Score 1436.5; DB 1; Length 682;  
Best Local Similarity 49.8%; Pred. No. 8-9e-92;  
Matches 288; Conservative 100; Mismatches 165; Indels 25; Gaps 6;

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QY 11 ESSPAPSKARKLLP-----VLDPGDDYVWMLNTMVPFVWNLIIIVGRACFPDLOHXY 65
DB 110 QSAAPADAPKCTFKERWEGFVVSQSDDIYVWLFALASLVNMTLVARACFDQDLQDEN 169
QY 66 LVAMVLVDYSDLLYLDMVVRFHGTGLEQGLIIVDKGRISRYVWTSGFFDLASLMP 125
DB 170 FFLWGLDVLGVYIYLDICRLRGTGYLEQGLIIVDKLRNRYRTLOFKLDPLSLT 229
QY 126 DVVYVRLGPHPTTLRLNRLPRLPRLPRLPRLPRLPRLPRLPRLPRLPRLPRLPRL 185
DB 230 ELLFVLTG-YVQLFRNRLRLRFRMFEFDRTRTETNPANARICNLIIYIIVIHMANC 288
QY 166 LVFALSRVYLGFRDAMVYDPAQPGFERLRQYLSFVFSTLITLVGDPPTPARREBYL 245
DB 289 IYVTSKALGSSDPTVWVSGQN---KTLSPCYVCFVWSTLTLTITGMPPVVDEEYV 344
QY 246 FMVGDPELLAVMGFATIMSGMSVIVYNNMTADAFYPDHALVKKYMKLQHNKRLERRVD 305
DB 345 FVYVDFLIGVLLFATIVGVSGISMNNAARAEFGORVDAIKQYNNFRVNSDMERVIK 404
QY 306 WYQHLQINKMTNEVALIQHLPERLRAEVAHSVHLSLRVQIPONCEASLLEBYLKLQ 365
DB 405 WFDYMTNKKTVDEQEVLLKLPDLKRAEIAINVHDLTKKRIIPDCEAGLLVEVLKLQ 464
QY 366 POTVSGEVYVCKGDIQGMYYIRREGQLAVVADDTQYAVAGAGYRGEISIIINIKGM 425
DB 465 PQVYVPGDITCKRGDIQGMYYIRREGQLAVVADDTQYAVAGAGYRGEISIIINIKGM 524
QY 426 SGNRRNTANIKSLGSDLPCLSKEDLREVLSEYPOAQTIIEEKGREILLKMKLDVNA 485
DB 525 MGNRRNTANIKSLGSDLPCLSKEDLREVLSEYPOAQTIIEEKGREILLKMKLDVNA 584
QY 486 EIALQEAATESRLGLDQDLDTQTFARLLAELESSALKIAYRIERLEWQ---TREWMP 542
DB 585 GLGVLD-TEEKVERLDASLDIILQTRFARLLGFTSTQRLKORITALERQLCHTGLIS 643
QY 543 EDLAR-----ADDEGEPEEGTSKDEGRASOE 569
DB 644 DNEAGEHAGVPTHTHADIHAQPEHTRTSAETNSEE 681

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## RESULT 15

S52072  
DmCNGC protein - fruit fly (Drosophila sp.)  
C:Species: Drosophila sp.  
C:Date: 14-Jul-1995 #sequence\_revision 21-Jul-1995 #ext\_change 16-Jul-1999  
C:Accession: S52072  
R:Baumann, A.; Frings, S.; Godde, M.; Seifert, R.; Kaupp, U.B.  
EMBO J. 13, 5040-5050, 1994  
A:Title: Primary structure and functional expression of a Drosophila cyclic nucleotide-  
A:Reference number: S52072; MUID:95045396; PMID:7957070  
A:Accession: S52072  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-665 <BAU>  
C:Genetics:  
A:Gene: FlyBase:Cng  
A:Cross-references: FlyBase:FBgn0014462  
C:Superfamily: cyclic nucleotide-gated channel; CAMP receptor protein cyclic nucleotide-  
F:429-553/Domain: CAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 41.3%; Score 1235; DB 2; Length 665;  
Best Local Similarity 47.1%; Pred. No. 8-3e-78;  
Matches 243; Conservative 98; Mismatches 165; Indels 10; Gaps 2;

